



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 174742

TO: Sean McGarry
Location: rem-2d19/2c18
Art Unit: 1635
Wednesday, December 28, 2005

Case Serial Number: 10/774974

From: Deirdre Arnold
Location: Biotech-Chem Library
REM 1A64
Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards,
Deirdre Arnold

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 24, 2005, 00:53:51 ; Search time 13 Seconds
(without alignments)
753.883 Million cell updates/sec

Title: US-10-774-974-2

Perfect score: 7500

Sequence: 1 MMQGYTCHMSFHPGCGPCR.....MRWERHQREPDDETIKK 1374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA New.*
- 1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pap.*
 - 2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pap.*
 - 3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pap.*
 - 4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pap.*
 - 5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pap.*
 - 6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pap.*
 - 7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pap.*
 - 8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	276	3.7	948	US-10-523-477-14	Sequence 14, Appl
2	260.5	3.5	245	US-10-793-626-1658	Sequence 1658, Ap
3	221.5	3.0	228	US-11-074-176-136	Sequence 136, App
4	221	2.9	1560	US-11-059-982-1	Sequence 1, Appli
5	211	2.8	244	US-10-467-657-2638	Sequence 2638, Ap
6	207	2.8	795	US-10-770-726-49	Sequence 49, Appl
7	190	2.5	1823	US-10-995-561-988	Sequence 988, App
8	190	2.5	2102	US-10-995-561-990	Sequence 990, App
9	190	2.5	2108	US-10-995-561-989	Sequence 989, App
10	190	2.5	2157	US-10-995-561-991	Sequence 991, App
11	175.5	2.3	175	US-10-821-234-1074	Sequence 1074, Ap
12	174	2.3	1970	US-10-821-234-1611	Sequence 1641, Ap
13	173	2.3	1532	US-10-821-234-914	Sequence 914, App
14	171	2.3	1178	US-11-044-899-29	Sequence 29, Appl
15	170.5	2.3	639	US-10-821-234-907	Sequence 907, App
16	168	2.2	580	US-10-995-561-987	Sequence 987, App
17	168	2.2	5179	US-11-108-172-1068	Sequence 1068, Ap
18	167.5	2.2	1187	US-10-821-234-955	Sequence 955, App
19	163	2.2	2432	US-10-821-234-899	Sequence 899, App
20	162	2.2	572	US-10-821-234-1290	Sequence 1290, Ap
21	155	2.1	186	US-10-508-263-111	Sequence 111, Appl
22	153.5	2.0	438	US-11-140-417-2	Sequence 2, Appli
23	153.5	2.0	4384	US-10-821-234-1120	Sequence 1120, Ap
24	152	2.0	509	US-10-821-234-1093	Sequence 1093, Ap
25	150.5	2.0	456	US-10-477-507A-2	Sequence 2, Appli

26	148.5	2.0	963	6	US-10-467-962B-2	Sequence 2, Appli
27	148	2.0	552	6	US-10-821-234-1022	Sequence 1022, Ap
28	146.5	2.0	793	7	US-11-060-914-2	Sequence 2, Appli
29	146	1.9	564	7	US-11-186-284-199	Sequence 199, App
30	146	1.9	1163	7	US-11-044-899-2	Sequence 2, Appli
31	145	1.9	1163	7	US-11-044-899-30	Sequence 30, Appl
32	144.5	1.9	273	6	US-10-821-234-1203	Sequence 1203, Ap
33	144.5	1.9	432	7	US-11-140-417-4	Sequence 4, Appli
34	143	1.9	676	7	US-11-135-855-28	Sequence 28, Appl
35	143	1.9	717	7	US-11-135-855-29	Sequence 8, Appli
36	142	1.9	356	7	US-11-143-986-8	Sequence 9, Appli
37	142	1.9	356	7	US-11-143-986-9	Sequence 110, App
38	141.5	1.9	160	6	US-10-508-263-110	Sequence 8, Appli
39	141.5	1.9	1516	6	US-10-220-824-8	Sequence 56, Appl
40	141	1.9	2011	7	US-11-080-991-56	Sequence 2, Appli
41	140.5	1.9	1618	6	US-10-984-645-2	Sequence 921, App
42	140	1.9	658	6	US-10-821-234-921	Sequence 1144, Ap
43	139.5	1.9	919	6	US-10-821-234-1144	Sequence 2, Appli
44	139	1.9	530	7	US-11-088-634A-2	Sequence 905, App
45	138	1.8	697	6	US-10-821-234-905	

ALIGNMENTS

RESULT 1
US-10-523-477-14
; Sequence 14, Application US/10523477
; Publication No. US20050266406A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MAXS AS MODIFIERS OF THE AXIN PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX03-051C-US
; CURRENT APPLICATION NUMBER: US/10/523,477
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US 60/401,534
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/411,153
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-523-477-14

Query Match		3.7%;	Score 276;	DB 6;	Length 948;
Best Local Similarity		23.0%;	Pred. No. 2.7e-10;		
Matches 149;		Conservative 61;	Mismatches 208;	Indels 230; Gaps 31;	
QY	27	ARPSA--PSFRPQNLRLHPPQPPVQYQYEPFSA-----PSTTFGNSPAPNLP	PPR 75		
DB	320	ARPGGRRPGWEHNSN-KLGYLVSPPPQPIRGRSVCYRSINRGHHSERSQTCQFS-LPAT	377		
QY	76	PDVFVPPPMPSAOGPLPPCPIRPPFNHQMHPFVPFPCFPMPMPCPNPPVPGA	135		
DB	378	PVFVPVPPP-----PLYPPPP-----HTLFLP-----PGVPPQSPQFP--PGQ	415		
QY	136	PRGQGTFFPMWPPSPMHPHPPPPVMPQQVN-----YQYPP-----	170		
DB	416	PPPAG---YVPPPPGPP-PAPANLSTPWVSSGVQTAHSNTIPTQAPPLSRFFEYRQR	471		
QY	171	-----GYSHHNFPFPPSFNS	184		
DB	472	LKEEEKKKSLDEFTNDFAKELMEYKKIQKERRSFRRSKSPYSGSSYSRSTYSKRS	531		
QY	185	FQNNPSSFLPANNSSSPHRLHPYPLPKASERSPERLKYDHRHSDHSHGGERH	244		
DB	532	GSTRSRYSRFSRSHSRYSRSPYP-----RRGRGKSRNY---RSRSRSHG---YH	578		
QY	245	RLSDRRRCGRSPDRRQDSRYSDYD-RGRTPSRHSYRSRERER-----	289		


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QY 62 ---TFNS-----PAPNLPDRDFVPPPPMPPSAQ---GPLPPCPPIRPPFNH----- 105
Db 833 GIFVIONQLGVPPPAFNPAFTAG--PPQPPLRPQSPPEGLPPAPHPAPPPSTTSASVAS 890
QY 106 ---QMRHPPVPPCPPPMPPMPCFNPPVPCAPPQCGTFPPMPPMPPMPPMPPMPPMPPMPP 157
Db 891 SSETSRLPAPTSDQLQPPPPGPHKSTP--PTL-----HLVPEAPPPPPPTPTQ 944
QY 158 ---PVMPPQ-----PVMPPQ-----VNYQ 167
Db 945 MVTTTTPPALPQPKALLERFHQVPSGIILQNKAGAPAAPOTSTSLGPLTSPAASVLVSGQ 1004
QY 168 YPGY-----SHNFP-----PPSFNSQONPPSSFLPSAN-----NSSSPHRHLPPYP 211
Db 1005 APSGTTAPSHAPAPMAATGLPPLPAENKAFASNLPTLNVAKAASSGPGKPSGLQYE 1064
QY 212 ---LPAKPSERSRSPER--LKHVDDHR-----HRDHSHG-----RGRHRSLDRR--BRGRS 255
Db 1065 SKLSGLKKPPTLQPSKEACFEHLHKHOGSVLHPDYKTAPPSPEDALHRLLPVHVYOGAL 1124
QY 256 PRRRQDSRYRSDYDRGRTSPRHSYRERERERHRH-----DNRR--SPSLE----- 304
Db 1125 PS-----PSDYHKVDEEFETVSTQLLKRTQMLNKYRLLLLESRRVSPSAEMWID 1176
QY 305 -----RSYKKEYRSGSYGLSVVPAGCTPGLPGLIKNVTSWAP 346
Db 1177 RMFIQEBKTTALDKLAKPKDEYVSSRSLSGLPTAASSEG--HRLPGH--GPLSSSAP 1232
QY 347 -----PLEIVNHRSPSRKKRAREEEDKRWSDNOSGDKNYTSIKEKEPEETM 396
Db 1233 GASTQPPPHLPKLVIRHGAGGSPVTVWARASSLSSSSSSSAASLDADEGDP---M 1289
QY 397 POKNE-----EBEELLKPYW-----IRCHSENYSDDPMDQVG----- 431
Db 1290 PSNRPPIKTYEARSIGLKLKIQEAGLSKVHVNTALDPVHPQPPPPATLKVABPPRP 1349
QY 413 -----PSTVVGTSR-----LRDLVKFEEELGSRQEK-----AKAR-- 463
Db 1350 PPPPPPTGOMNGTVDPHPHPAAPERKPLGTAPHCPRLPKTYREN-----VGGPGA 1400
QY 432 -DSTVVGTSR-----LRDLVKFEEELGSRQEK-----AKAR-- 463
Db 1401 PEGTPAGRAGGSPAPLPKVDKATSGLIREL-AAVEDELYQRLMKGPPEPPAASAAQGT 1459
QY 464 --PPWPPPTKLDLEDLESSESCEDESDSTCSSSDSEVFDVIAE 507
Db 1460 GDPDWEAP-----GLPPAKRKSESPPVDVQASFSSDSPQDDTLTE 1499

RESULT 5
US-10-467-657-2638
; Sequence 2638, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 2638
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2638
```

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Query Match 2.8%; Score 211; DB 6; Length 244;
Best Local Similarity 28.3%; Pred. No. 6.7e-07;
Matches 68; Conservative 41; Mismatches 117; Indels 14; Gaps 6;

QY 1095 ROLIETSPVL--OKLTFEFAAIGVIFTHVRLLARAFTRTVGNHLTLGHNORMEFLGDS 1152
Db 2 RKTVMKDDVLKQQAHTAIQKLGAFRDMSLRLRALTHRS--HHAK--HNEFEFVGDS 56
QY 1153 IMQLVATEYLFTHPPHGHGLTLRSSLVNNRTOAKVABELGMQEQVATINDTKRPVGL 1212
Db 57 ILNYTVARMFLFOAFPPLKTEGELSRLASLVNEGVLAEAAEMVNGDGLYLGAELKSSGF 116
QY 1213 RYKT-LADLLESFIAALYTDKOLEYVHTFMNVCFPRLKKEPILNQDWNDPKSOLOQCCLT 1271
Db 117 RRSIILADAMEAMFAVSDADFNTAKVKVRHLFAERVRADFQNAKDKGTALQEA--- 173
QY 1272 LRTEGKEPDIPLYKTLQTVGPSHARTYTVAVYFKGERIG-GKGPSITQQAEMGAAMDAL 1330
Db 174 --LQARRFALPKYRIBEQIGHADDSMFVISCDELGELGVCRAKGTSRKAQEAKEALK 231

RESULT 6
US-10-770-726-49
; Sequence 49, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 795
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-49

Query Match 2.8%; Score 207; DB 6; Length 795;
Best Local Similarity 26.4%; Pred. No. 5.3e-06;
Matches 89; Conservative 41; Mismatches 127; Indels 80; Gaps 13;

QY 214 KAPSRERSPERLKHYYD-----HRRDHS-----HGRGHRH-SLDORRE 251
Db 86 KPQQMSRKERKHHKDEKRRKRRHSASGEGKHARVKEKEREHRRKHREEQDKAR 145
QY 252 RGRSPDRRQDSRYRSDYDRGRTPTSPRHSYERSR-----ERER-----ERHHR 295
Db 146 REWERQKREMAHRSRRERDRLEQLERKREKRMREQKEQKEQKEREERRAEERRKER 205
QY 296 DNRSPSL-ERSYKKEYKRSYGLSVVPEPAGCTPGLPGLIKNVTSWAPPLEIVNHR 354
Db 206 EARREYSAHRTWREDYSDVKASHWSRSP-----PRPRERFELGDKRP-----GEA 254
QY 355 SPSREKKRARWEEK-----DRWSDNOSGCKNYTSIKEKEPEETMPDKNEEEEEELKP 410
Db 255 RPARAQKPAQLKEEKWNERDLISDLODISDKRSTSSAASSSSAASSGSGSEEEEEEE 310
QY 411 VMIRCTHSENYSSYSDPMDQVGVSTVGTSLRDLVDKFEELGSGRQEKAKAARPPWPPK 470
Db 311 -----EEEEEG-STSESEEEEEEEEEEEEEETGNSNEEA-SEQSAEVS 354
QY 471 TKLDEDLSESSS-----ECSEDESDSTCSSSDSEV 501
Db 355 EEMSEDEERENHLLVPESRFDRDGSGBAEAEV 391

RESULT 7
US-10-995-561-988
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[illegible]

QY 436 -----VTSRLRLDYDKPEELGSRQEKAKAARPPWPPKTKL-----DEGLE--- 478
Db 1182 GERPRRRHGRAQQODKPPFRFR---LKQERENAAARGSEKPSLTLPASAPGPEEALTTV 1238
QY 479 -----SSSECEDEDETCSSSDSEVDFVIAEIKR---KKAHPDRLHD 520
Db 1239 TVAPAPRAAAKSPDLNSQNSDOANEWEETASESSD-----FTSRRGDKKEAPPPVLLT 1292
QY 521 ELWYNDPGQMDGPKCKCSAKAR 543
Db 1293 PRAVGTGPGGGGAVPGISAMSR 1315

RESULT 9
US-10-995-561-989
; Sequence 989, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 989
; LENGTH: 2108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-989

Query Match 2.5%; Score 190; DB 6; Length 2108;
Best Local Similarity 21.2%; Pred. No. 0.00022;
Matches 170; Conservative 47; Mismatches 258; Indels 328; Gaps 39;

QY 19 PRGRG-GHGARSA-----PSFRPNLRLHLPQPPVQYQYE----- 54
Db 563 PKGDGIGTPRQPPSQGLGYPKYKSLPRFRFORQOEQLLKQOQHQOQOQSGAPPTV 622
QY 55 PPSAPS-TTFSNSPAPNPLPP-----RPDFVFPFPPMPPSAQGP----- 92
Db 623 PPSPPQVTLGAVPAPQAPPPPKALYPCALGRPPPPMPPMPPMPPMPPVYDPRLLQG 682
QY 93 LPCCIRP-----PPFNH-----QMRHPPVPVPCF----- 117
Db 683 RPPLDFYPPGVHPSGLVPRERSDGSSEPPDRHAPAMLRERGTTPVDPKLAWGVDVFT 742
QY 118 -----PPMPPMP-----CPNN-----PPV----- 132
Db 743 ATPAPRPLTSLRQAADDDKGRSETPPVFPFPPPYLASYPGFPENGAGPPISRFPLE 802
QY 133 -PGA-----PPCQGTFFPFPMPSPMHP-----PPPPV 159
Db 803 EPGPRPLPMPGSDVAKIQTPTPKKPKKEBTAQLTGPEAGKPKARGVSGGQGGPPPPR 862
QY 160 MPQVNYQY--PPGYSHNFPPSPFNSFQNNSSFLPSANNSSSHFRHLPPVPL----- 212
Db 863 RESRTETRWGPRGSGRRGIPPEEPCA---PPRAGPIKPPPPPTKVEELPKPLEQDGE 919
QY 213 -PKAFSERRSRLK-----HYDDHRRHDSH-----GRGE 242
Db 920 TKPP-----KPDPLKITGKLGKPKETPPNGNLSAPRLRRDYSYERVGTPSCRGGRGE 975
QY 243 ---RHSRLDRRGRSPDRRQDSR-----YRSD-----YDRGTPSRHSR-- 280
Db 976 YFARGRGFTGYGGRGARSRFRSFRYREFRGDGRGGGTGPNHPPAPRGRTASSETRSE 1035
QY 281 ---YERSRERER-----HHRNRRSPSLSERSYKKEYKSGRSYGLSVVPEPAGCTP 331
Db 1036 GSEYBEIPKRRQRGSETGSETHESDLAPSDKEAPTPE-----GTLTQVPLAPPPPPGAPP 1091

QY 332 E-LPGEIKWTDSWAPPLEIVNHRSPSRKKRABW-----EERKDSNDSQSGKQKNT 385
Db 1092 SPAPARFTARGRVTPRGV-----PSR-----RGRGGRPPPPQVCPGMSPPAKSLAPK--- 1140
QY 386 SIKEKEPEETMDKNEEBEELLPWIRCTHSENYSSDPMDOV-----GDSV----- 435
Db 1141 ----KPTGPLPPSKEPLKEKLI-----PGPLSPVARGSGSGSNVGMED 1181
QY 436 -----VTSRLRLDYDKPEELGSRQEKAKAARPPWPPKTKL-----DEGLE--- 478
Db 1182 GERPRRRHGRAQQODKPPFRFR---LKQERENAAARGSEKPSLTLPASAPGPEEALTTV 1238
QY 479 -----SSSECEDEDETCSSSDSEVDFVIAEIKR---KKAHPDRLHD 520
Db 1239 TVAPAPRAAAKSPDLNSQNSDOANEWEETASESSD-----FTSRRGDKKEAPPPVLLT 1292
QY 521 ELWYNDPGQMDGPKCKCSAKAR 543
Db 1293 PRAVGTGPGGGGAVPGISAMSR 1315

RESULT 10
US-10-995-561-991
; Sequence 991, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 991
; LENGTH: 2157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-991

Query Match 2.5%; Score 190; DB 6; Length 2157;
Best Local Similarity 21.2%; Pred. No. 0.00022;
Matches 170; Conservative 47; Mismatches 258; Indels 328; Gaps 39;

QY 19 PRGRG-GHGARSA-----PSFRPNLRLHLPQPPVQYQYE----- 54
Db 618 PKGDGIGTPRQPPSQGLGYPKYKSLPRFRFORQOEQLLKQOQHQOQOQSGAPPTV 677
QY 55 PPSAPS-TTFSNSPAPNPLPP-----RPDFVFPFPPMPPSAQGP----- 92
Db 678 PPSPPQVTLGAVPAPQAPPPPKALYPCALGRPPPPMPPMPPMPPMPPVYDPRLLQG 737
QY 93 LPCCIRP-----PPFNH-----QMRHPPVPVPCF----- 117
Db 738 RPPLDFYPPGVHPSGLVPRERSDGSSEPPDRHAPAMLRERGTTPVDPKLAWGVDVFT 797
QY 118 -----PPMPPMP-----CPNN-----PPV----- 132
Db 798 ATPAPRPLTSLRQAADDDKGRSETPPVFPFPPPYLASYPGFPENGAGPPISRFPLE 857
QY 133 -PGA-----PPCQGTFFPFPMPSPMHP-----PPPPV 159
Db 858 EPGPRPLPMPGSDVAKIQTPTPKKPKKEBTAQLTGPEAGKPKARGVSGGQGGPPPPR 917
QY 160 MPQVNYQY--PPGYSHNFPPSPFNSFQNNSSFLPSANNSSSHFRHLPPVPL----- 212
Db 918 RESRTETRWGPRGSGRRGIPPEEPCA---PPRAGPIKPPPPPTKVEELPKPLEQDGE 974
QY 213 -PKAFSERRSRLK-----HYDDHRRHDSH-----GRGE 242
Db 975 TKPP-----KPDPLKITGKLGKPKETPPNGNLSAPRLRRDYSYERVGTPSCRGGRGE 1030

QY 243 ---RHSLDRRGRSPDRRRQDSR-----YRSD-----YDRGETPSRHS- 280
Db 1031 YFARGRGFRGTYGGRGRGARSRFRSRYRFRGDDGRGGTGGNHPAPRGRGTATRSSE 1090
QY 281 ---YRSRERER-----HRHNRSPSLRSYKKEYKRSYGLSVVPEPAGCTP 331
Db 1091 GSEYBEIPKRRQRGSETSETHESLAPSDKEATPK-----GTLTQVPLAPPFGAPP 1146
QY 332 E-LPGELIKNTDWAAPLBIVNHRSRSPREKKAARW-----EEXKRWSONSGKDKNVT 385
Db 1147 SPAPARFTARGRVFTFPGV-----PSR---RGRGGGRPPQVCPGWSPPAKSLAPK--- 1195
QY 386 SIKEBPEPTMDKNEEBEELLKPWIRCTHSENYSSDPMDOV-----GDSTV--- 435
Db 1196 ----KPTGFLPPSKPELKEKLI-----PCPLSPVARGSGNGSNVGMED 1236
QY 436 -----VGTSLRLDLYKFEELSGROEKAKAARPPWPEPKTKL-----DEGLE-- 478
Db 1237 GERPRRRHGRAQQQDKPRFR---LQERENAAKRGSEKSLTLPASAPGPEALITV 1293
QY 479 -----SSSECEDEDESDSSSDSEVDFVIAEIKR---KXAHPRDLHD 520
Db 1294 TVAPAPRAAAKSPDLNSQNSQANEWEETASESSD-----FTSERRGDKEAPPVLLT 1347
QY 521 ELWYNDPGQWNDGPLCKCSAKAR 543
Db 1348 PKAVGTFPGGGGGAVFGISAMSR 1370

RESULT 11

US-10-821-234-1074
; Sequence 1074, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1074
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1074

Query Match 2.3%; Score 175.5; DB 6; Length 175;
Best Local Similarity 29.2%; Pred. No. 7.9e-05;
Matches 57; Conservative 13; Mismatches 52; Indels 73; Gaps 12;
QY 62 TFSNSPAPNPLPRPRDFVPPPPMP-PSAQGLPPCPIRPPFPHQMRHPPFVPPCFPPM 120
Db 24 THLNMNPNAGQPGPN--PYPPNIGCGGSPNAPHPPIPPF----- 63
QY 121 PPMPCNNPPVPGAPPGQCTFFPMMPSPSMHPHPPPPVMPQ-QVNYQVPPGYSHNFPP 179
Db 64 -PPGPC---PPPGAGHGNPAF-----PPGGPHFVPPQGYPGCQPIGPVPPPY-----PP 110
QY 180 PSFNSQNNPSSFLPSANNSSPHFRHLPPYLPKAPS-----ERRSPRLK----- 226
Db 111 PA-----PG--IPPVN-----PLAFGVGPAVIVDKMKQKKAHK 146
QY 227 -HYDDHRHRDHSRGR 240
Db 147 MHKHQKHKKYKHGK 161

RESULT 12
US-10-821-234-1641
; Sequence 1641, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1641
; LENGTH: 1970
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1641

Query Match 2.3%; Score 174; DB 6; Length 1970;
Best Local Similarity 27.8%; Pred. No. 0.0021;
Matches 64; Conservative 27; Mismatches 101; Indels 38; Gaps 13;
QY 19 PRGRGHGARPAPSRFRPONLRLHPQPPVQYQYEP-----PSAPS---TTFNSNP-A 68
Db 1602 PRSPGGY--TPQSPSYSPS-----PSYSPTSPSYSPSPTSPSYSPSYSPSPTS 1654
QY 69 PNFLLPRDFVPPPPMPSPSAQGLPPCP-IPPPPHQMRHP--FPVPPCFPPMPDP--- 122
Db 1655 PSYSPTSPSYSPSPTSPSYSPSPTSPSYSPSPTSPSYSPSPTSPSYSPSPTS 1714
QY 123 ---PMPCPNPNPV-PCAGPGQCTFFPMMPSPSMHPHPPPPVMPQVNYQ-YPPGY--HH 175
Db 1715 PTSPSYSPSPTSPSYSPSPTSPSYSPSPTSPSYSPSPTSPSYSPSPTSPSYSPSPTS 1774
QY 176 NFPFSPFNSFQNNPS-----SFLPS--ANNSSPHFRHLPPYLPKAPS 217
Db 1775 NYTPTSPNYSPSPTSPSYSPSPTSPSYSPSPTSPSYSPSPTSPSYSPSPTS 1824

RESULT 13
US-10-821-234-914
; Sequence 914, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 914
; LENGTH: 1532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-914

Query Match 2.3%; Score 173; DB 6; Length 1532;
Best Local Similarity 28.3%; Pred. No. 0.0017;
Matches 82; Conservative 15; Mismatches 97; Indels 96; Gaps 18;
QY 13 HPGRCGPRGRGG-----HGAR-PSAPSRFQNLRLHPQPPVQYQYEP-----P 56

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Db 785 HQG---PRGQLTGMGIRGPGSPGDKPKGLTGQGP-----QGLPCTGPRGKGP 837
Qy 57 SAPSTTFSNAPNLFPRDFVP--FPPMPPSAQGLPPCPTRPPFPNHQ-----NRHP 110
Db 838 GAPCKIVTSGSSMLTVPGPPGPGGAMGPPGPGAGPAGL-----PGHQEVLNLQGP 893
Qy 111 FVPPCPFPMPMPPCNNPVCAPGCG-----TPPMPMPSPMHP 156
Db 894 -PGPP--GPRGPPGFSIPGPPGPRGEGLPGGPGGFLNSFTFLFGPPGPPG 950
Qy 157 P-----PVMPQ-----QVNYQPPGYSHNFP-----PS 181
Db 951 PKGQGGPPGRHQEGQLGCFSTSGSSSGMLNLQGGP-----PGPQGPKGDKGDFG 1004
Qy 182 FNSQNNPSSFLPSANNSSPHRHLPPYPL-PAK--SRRRSPERLKH 228
Db 1005 VPGALGPSG--PSEGGSSMTVYSGPPGPPGPPGSISSGQEQY 1052

RESULT 14
US-11-044-899-29
; Sequence 29, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT FILING DATE: 2005-01-26
; PRIOR FILING DATE: 2001-09-24
; PRIOR FILING DATE: 2001-09-24
; PRIOR FILING DATE: 1999-11-05
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 1178
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(1178) at all Xaa position
; OTHER INFORMATION: Xaa = any amino acid
US-11-044-899-29
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Query Match 2.3%; Score 171; DB 7; Length 1178;
Best Local Similarity 21.2%; Pred. No. 0.0017;
Matches 120; Conservative 60; Mismatches 217; Indels 170; Gaps 23;

Qy 56 SAPSTTFSNAPNLFPRDFVPFPPMPPSAQGLPPCPTRPPFPNHQMPFPVPP 115
Db 69 PTAPA---AGAPLMDF---GNDFV-----PPAPGFLPAAP-----PVAP 102
Qy 116 CFPMPMPPCNNPVPVCGAPPQGGTFPMPMPSPMP--HPPPPVMPQVNYQPPGYS 173
Db 103 ERQPSWDPSPSVSTVAPSPLSAAVSPKLPDEDEPPAPPPPP--PASVSPAAPVMT 160
Qy 174 HNFPPPPSFNSFQNFPSFLPSANNSSPHRHLPPYPLPKA-PSRRRSPERLKHDDHR 232
Db 161 -----PPAPAPAAPSTPAAPK----- 178
Qy 233 HRDHSRGGE-----RHSRLRRR-GRSPRRQDSYRSDYRGTRPSRHSYRS 284
Db 179 -----RGSSGAVVXXXXKIMDLKEQPGNTISAGQED-----PPSVLLETAAS 220
Qy 285 RERERHRHRDRNRSPSLERSYKKEYSGLSVVPEPAGCTPELPGELIKNTDSW 344
Db 221 -----XPSUSPLSAASGKEHYLGNLSTVLPTGTQENNVSEASKEVSEK 265
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Qy 345 APPLIENVHRSPPREKKRAREEKKORWSNQSGKDKNTYSIKEKEPPTMDKNEEE 404
Db 266 AKTLII-----DRDLTFESELSEYSEMGSSFSVSPKAESAVIVANPREIIVKNKDEE 317
Qy 405 EELLKPWVIRCTHSENYSSDPMDQVGDSTVVGTSRLRLDYD--KPEEELGSRQEK--K 460
Db 318 EKLVSN---NILXQQLPALTALVKEDVSVSEKAKDSFNKRVAVAPMEYADFK 374
Qy 461 AARPPWPPPKTLDELESS---ESECSEDESTCSSSDSEVDFVIAIKRKAHPDR 517
Db 375 PFERVVEVSKSDSDMLAAGGKIESNLKSKVKCF--DSLEQTNHEKDGESS 427
Qy 518 LHDELWYNDPGQWMDGFLCKCSAKARTGIRHSIYPGEBAIKCRPMTNNAGRLPHYRIT 577
Db 428 NDDTSFPSTPEGIKD-----RSG-----AYITCAP-----FNPAAT 458
Qy 578 VSPPTNF--LTDRTPTVIEYDDHEVIFE 602
Db 459 ESIATNIFPLEDPTSENXTDEKIEE 485
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RESULT 15

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US-10-821-234-907
; Sequence 907, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT FILING DATE: 2004-04-07
; PRIOR FILING DATE: 2004-04-07
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 907
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-907
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Query Match 2.3%; Score 170.5; DB 6; Length 639;
Best Local Similarity 34.7%; Pred. No. 0.00084;
Matches 60; Conservative 20; Mismatches 72; Indels 21; Gaps 9;
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Qy 218 ERSPERLKHYYDDHRDHSHGGERHRSIDR---RERGRSPRRQDSYRSDYRGRT 274
Db 423 ERPGPSPLPHRD--RDRERERRRERSRBRDKERERRRSDRRRR--SRSDKEBRR-- 478
Qy 275 PSRHSYERSRERERERHHRNRRSPSLERSYKKEYSGLSVVPEPAGCTPE-- 332
Db 479 -SRERSKDKDRKKRKSRSRERARR---ERERKEELRGG---GMAEPSEAGDAPDD 531
Qy 333 -LPGEIINKTDSWAPPLIENVHRSPPREKKRAREEKKORWSNQSGKDKNY 384
Db 532 GPPGEL--GPDGPDGPEE--KGRDRDRRRRSHRSRERDRDRDRDRDR 580
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Search completed: December 24, 2005, 01:03:14
Job time : 20 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 24, 2005, 00:51:00 ; Search time 52 Seconds
(without alignments)
2184.546 Million cell updates/sec

Title: US-10-774-974-2

Perfect score: 7500

Sequence: 1 MQQNTCHRMSPHGRGCRP.....MRWRHQREPDTEYDIKK 1374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5 COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/6 COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/PTUS COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7500	100.0	1374	2	US-09-900-4258-2
2	2463	32.8	466	2	US-09-900-4258-37
3	890	11.9	412	2	US-09-900-4258-3
4	496	6.6	115	2	US-09-513-999C-4635
5	316	4.2	553	2	US-09-949-016-7961
6	312.5	4.2	241	2	US-09-107-532A-5434
7	284.5	3.8	232	2	US-09-583-110-4554
8	284.5	3.8	236	2	US-09-107-433-4394
9	284.5	3.8	998	2	US-09-949-016-7757
10	277.5	3.7	232	1	US-08-869-674-2
11	277.5	3.7	232	2	US-09-213-010-2
12	277.5	3.7	232	2	US-09-213-011-2
13	271.5	3.6	386	2	US-09-461-774-10
14	267	3.6	243	2	US-08-965-087-2
15	264.5	3.5	1404	2	US-08-801-308-1
16	263	3.5	227	2	US-09-489-039A-11549
17	262	3.5	226	2	US-09-900-4258-6
18	262	3.5	971	2	US-09-248-796A-19531
19	260.5	3.5	245	2	US-09-710-279-1658
20	260.5	3.5	246	2	US-09-134-001C-4787
21	254.5	3.4	607	2	US-09-248-796A-19157
22	252	3.4	228	2	US-09-543-681A-7646
23	248.5	3.3	904	2	US-09-976-594-615
24	239.5	3.2	439	2	US-10-300-819B-21
25	239.5	3.2	865	2	US-09-281-766-19
26	239.5	3.2	865	2	US-09-612-858-19
27	239.5	3.2	865	2	US-09-957-995A-19

28	239	3.2	253	2	US-09-352-991A-29495	Sequence 29495, A
29	233.5	3.1	268	2	US-09-340-236-2003	Sequence 2003, Ap
30	232.5	3.1	1646	2	US-09-535-008-67	Sequence 67, Appl
31	232.5	3.1	1647	2	US-09-535-008-2	Sequence 2, Appl
32	232.5	3.1	1647	2	US-09-824-574-4	Sequence 4, Appl
33	232.5	3.1	1647	2	US-09-538-092-1172	Sequence 1172, Ap
34	232.5	3.1	1649	2	US-09-535-008-75	Sequence 75, Appl
35	232.5	3.1	1650	2	US-09-535-008-71	Sequence 71, Appl
36	232.5	3.1	1659	2	US-09-949-016-9752	Sequence 9752, Ap
37	232.5	3.1	1678	2	US-09-535-008-69	Sequence 69, Appl
38	232.5	3.1	1679	2	US-09-535-008-65	Sequence 65, Appl
39	232.5	3.1	1681	2	US-09-535-008-77	Sequence 77, Appl
40	232.5	3.1	1682	2	US-09-535-008-73	Sequence 73, Appl
41	230.5	3.1	254	2	US-09-553-863-18	Sequence 18, Appl
42	230.5	3.1	1909	2	US-09-590-968B-2	Sequence 2, Appl
43	230	3.1	666	2	US-09-050-739-70	Sequence 70, Appl
44	229.5	3.1	424	2	US-09-538-092-1338	Sequence 1338, Ap
45	228.5	3.0	259	2	US-09-438-185A-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1

US-09-900-4258-2
; Sequence 2, Application US/09900425B
; Patent No. 6737512
; GENERAL INFORMATION:
; APPLICANT: Wu, Hongjiang
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof
; FILE REFERENCE: IS155029/ISPH-0522
; CURRENT APPLICATION NUMBER: US/09/900,425B
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-900-4258-2

Query Match 100.0%; Score 7500; DB 2; Length 1374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MQQNTCHRMSPHGRGCRGCGHGRGARGARPSAFRPNQLRLHLPQQPPVQYQYEPSPAPS	60
DB	1	MQQNTCHRMSPHGRGCRGCGHGRGARGARPSAFRPNQLRLHLPQQPPVQYQYEPSPAPS	60
QY	61	TTFSNSPAPNPLPRPDPVFPFPPPPPSAQGLPPCPIRPPFNHQRHPPFVPPCFPPM	120
DB	61	TTFSNSPAPNPLPRPDPVFPFPPPPPSAQGLPPCPIRPPFNHQRHPPFVPPCFPPM	120
QY	121	PPMPCNNPPVPGAPPGGCTFFMPPSPHPPPPVPMQOVNTQYPGYSHNPPPP	180
DB	121	PPMPCNNPPVPGAPPGGCTFFMPPSPHPPPPVPMQOVNTQYPGYSHNPPPP	180
QY	181	SFNSFONNPSFLPSANNSSPHFHLPPYPLPKAPSERSSPERLKHYYDDHRRDHSR	240
DB	181	SFNSFONNPSFLPSANNSSPHFHLPPYPLPKAPSERSSPERLKHYYDDHRRDHSR	240
QY	241	GERHSLDRRGRGPDRRRQDSRYSDYDRGRTSPRHSYERSRERERHRRNR	300
DB	241	GERHSLDRRGRGPDRRRQDSRYSDYDRGRTSPRHSYERSRERERHRRNR	300
QY	301	PSLESYKKEYKRSYGLSVVPPAGCTPLPGELIKNTDSWAPPLIVNHRSPREK	360
DB	301	PSLESYKKEYKRSYGLSVVPPAGCTPLPGELIKNTDSWAPPLIVNHRSPREK	360
QY	361	KEARWEEKDRWSDNQSSGDKNYTSIKKEPEETMPDKNEEBEELLKPVWIRCTHSEN	420
DB	361	KEARWEEKDRWSDNQSSGDKNYTSIKKEPEETMPDKNEEBEELLKPVWIRCTHSEN	420

421 YSSDDMDQVGVSTVGTSLRLDLYDKFBEELGSRQEKAKAAPPPWEPKTKLDELESS 480
Db YSSDDMDQVGVSTVGTSLRLDLYDKFBEELGSRQEKAKAAPPPWEPKTKLDELESS 480
481 SESECEDESDSTCSSSDSEVFVIAEIKRKAHPDRLHDELWYNDPGQMDGPKCKCSA 540
Db SESECEDESDSTCSSSDSEVFVIAEIKRKAHPDRLHDELWYNDPGQMDGPKCKCSA 540
541 KARTGIRHSIYPGEBAIKPCRPMTNAGRLFHYRITVSPPTNFLTDRPTVIEYDDHEVI 600
Db KARTGIRHSIYPGEBAIKPCRPMTNAGRLFHYRITVSPPTNFLTDRPTVIEYDDHEVI 600
601 FEGFSMFAHAPLNIPLCKVIRENIDYTHFTEEMMPENFCVKGLFSLFLFRDILELY 660
Db FEGFSMFAHAPLNIPLCKVIRENIDYTHFTEEMMPENFCVKGLFSLFLFRDILELY 660
661 DWNKGLPDPEDSPCCPRFHFMPRFVFLPDGCKEVLMSHQILLYLLRCSKALVPBEEIA 720
Db DWNKGLPDPEDSPCCPRFHFMPRFVFLPDGCKEVLMSHQILLYLLRCSKALVPBEEIA 720
721 NMLQWEELEWQKVAEBCKGMIVTNPCTKPSVRAIDQDREQFNPDVITPPIIVHFGIRPA 780
Db NMLQWEELEWQKVAEBCKGMIVTNPCTKPSVRAIDQDREQFNPDVITPPIIVHFGIRPA 780
781 OLSYAGDPOYOKLWKSYYVKLRLHLLANSPKVKOTDKOKLAQREALOKIRQKNTMRREVTV 840
Db OLSYAGDPOYOKLWKSYYVKLRLHLLANSPKVKOTDKOKLAQREALOKIRQKNTMRREVTV 840
841 ELSQSQFWTKGIRSDVQCHAMMLPVLTHIRYHQCLMHLDKLIGYTFQDRCLLQAMTHP 900
Db ELSQSQFWTKGIRSDVQCHAMMLPVLTHIRYHQCLMHLDKLIGYTFQDRCLLQAMTHP 900
901 SHHLNFGMNDPHARNLSNCGIRQPKYGRKVVHMMRKKGINTLINMSRLGQDDPTPS 960
Db SHHLNFGMNDPHARNLSNCGIRQPKYGRKVVHMMRKKGINTLINMSRLGQDDPTPS 960
961 RINHNRLBFLGDVAVVEFLTSVHLIYLPSPLEGGATYRTAIVQNOHLAMLAKELEDP 1020
Db RINHNRLBFLGDVAVVEFLTSVHLIYLPSPLEGGATYRTAIVQNOHLAMLAKELEDP 1020
1021 FMLYAHGPDLCRSDLRHAMANCFEALIGAVYLEGSLEEAQKQFGRLLFNDPDLREVWLN 1080
Db FMLYAHGPDLCRSDLRHAMANCFEALIGAVYLEGSLEEAQKQFGRLLFNDPDLREVWLN 1080
1081 YPLHPLQLQEPNTDROLIETSPVLQKLTETFEAIGVIFTHVRLARAFTLRTVGFNHLTL 1140
Db YPLHPLQLQEPNTDROLIETSPVLQKLTETFEAIGVIFTHVRLARAFTLRTVGFNHLTL 1140
1141 GHNQREFLGDSIMQVATEYLFTHFPDHEHGLTLRLSSLVNNRTOAKVAEELGMOEYA 1200
Db GHNQREFLGDSIMQVATEYLFTHFPDHEHGLTLRLSSLVNNRTOAKVAEELGMOEYA 1200
1201 ITNDKTRPVGLRTKTLADLLESFIAALYTDKOLEYVHTFMNVCFPPRLKEFTLNQDND 1260
Db ITNDKTRPVGLRTKTLADLLESFIAALYTDKOLEYVHTFMNVCFPPRLKEFTLNQDND 1260
1261 PKSLOQCCLTLTREGKEPDIPLYKTLQTVGPHSHARTYTVAVYFKGERICGKGPSIQQA 1320
Db PKSLOQCCLTLTREGKEPDIPLYKTLQTVGPHSHARTYTVAVYFKGERICGKGPSIQQA 1320
1321 EMGAAMDALKYFPQMAHQKRFGRKYROELKEMRWEREHQEREPEDETIKK 1374
Db EMGAAMDALKYFPQMAHQKRFGRKYROELKEMRWEREHQEREPEDETIKK 1374

RESULT 2
US-09-900-425B-37
; Sequence 37, Application US/09900425B
; Patent No. 6737512
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.

; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof
; FILE REFERENCE: ISIS5029/ISPH-0522
; CURRENT APPLICATION NUMBER: US/09/900,425B
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 37
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-900-425B-37

Query Match 32.8%; Score 2463; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 2.4e-185;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 909 NPDHARNLSNCGIRQPKYGRKVVHMMRKKGINTLINMSRLGQDDPTPSRINHERL 968
Db 1 NPDHARNLSNCGIRQPKYGRKVVHMMRKKGINTLINMSRLGQDDPTPSRINHERL 60
QY 969 EFLGDVAVVEFLTSVHLIYLPSPLEGGATYRTAIVQNOHLAMLAKELEDPFMYAHGP 1028
Db 61 EFLGDVAVVEFLTSVHLIYLPSPLEGGATYRTAIVQNOHLAMLAKELEDPFMYAHGP 120
QY 1029 DLCRESDLRHAMANCFEALIGAVYLEGSLEEAQKQFGRLLFNDPDLREVWLNYPHLPLQL 1088
Db 121 DLCRESDLRHAMANCFEALIGAVYLEGSLEEAQKQFGRLLFNDPDLREVWLNYPHLPLQL 180
QY 1089 QBPNTDROLIETSPVLQKLTETFEAIGVIFTHVRLARAFTLRTVGFNHLTLGHQORMEF 1148
Db 181 QBPNTDROLIETSPVLQKLTETFEAIGVIFTHVRLARAFTLRTVGFNHLTLGHQORMEF 240
QY 1149 LGDSIMQVATEYLFTHFPDHEHGLTLRLSSLVNNRTOAKVAEELGMOEYAITNDKTKR 1208
Db 241 LGDSIMQVATEYLFTHFPDHEHGLTLRLSSLVNNRTOAKVAEELGMOEYAITNDKTKR 300
QY 1209 PVGLRTKTLADLLESFIAALYTDKOLEYVHTFMNVCFPPRLKEFTLNQDNDPKSLOQCC 1268
Db 301 PVGLRTKTLADLLESFIAALYTDKOLEYVHTFMNVCFPPRLKEFTLNQDNDPKSLOQCC 360
QY 1269 CLTLRTREGKEPDIPLYKTLQTVGPHSHARTYTVAVYFKGERICGKGPSIQQAEMGAAMD 1328
Db 361 CLTLRTREGKEPDIPLYKTLQTVGPHSHARTYTVAVYFKGERICGKGPSIQQAEMGAAMD 420
QY 1329 LEKYNPPQMAHQKRFGRKYROELKEMRWEREHQEREPEDETIKK 1374
Db 421 LEKYNPPQMAHQKRFGRKYROELKEMRWEREHQEREPEDETIKK 466

RESULT 3
US-09-900-425B-3
; Sequence 3, Application US/09900425B
; Patent No. 6737512
; GENERAL INFORMATION:
; APPLICANT: Wu, Hongjiang
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof
; FILE REFERENCE: ISIS5029/ISPH-0522
; CURRENT APPLICATION NUMBER: US/09/900,425B
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-900-425B-3

Query Match 11.9%; Score 890; DB 2; Length 412;
Best Local Similarity 43.1%; Pred. No. 1.4e-61;
Matches 181; Conservative 85; Mismatches 136; Indels 18; Gaps 7;

QY 944 TLINMSRLGQDDPTPSRINHERLFLGDVAVVEFLTSVHLIYLPSPLEGGATYRTAI 1003

2	SLFNIMKGTSGGB-----ILHNERLEYGDAVVELIVSHHLYFMLTHFFEGGLATYRTAL	57
1004	VQNOHLAMLAKCLELDPFMYAYGPDLCRESDLRHAMANCFEALIGAVYLEGSLBEAAKQL	1063
58	VQNRNLATLANCKRIDEMLOYSGHADLIINVAEPKHALANAFVAAIAIYLDGGLAPCDVI	117
1064	FGRLLF--NDPDLREVWLNYPHLPIQLQEPNTDROLIETSPVLQKLTFFEEAIGVIFTHVR	1122
118	FSKAMYGHQPVLEKEWDHINEHELKREDPOGDRDLSFITLTSTFHALBEERLGIQFNIR	177
1123	LLAAFTLRTVGNHLLTGHNQRMPEFGDSIMQLVATEYFIPIHPDHHGHLTLRLSSL	1182
178	LLAKAPTRRNI PNNDLTKGHNQRLWLGDSVLQLIVSDFLVRRPPYHHGHMSLRSTSLV	237
1183	NNRTOAKVABELGMQEVAIYNDTKTRPV---GLRTKTLADLLSFIALYTDKDLLEVHT	1239
238	SNQTQAVVCCDLGTFEVI-----KAPYKTPELKLDKADLVEAFICALVVDRGIEHCA	292
1240	PMWVCPPLRKEPIFLNQDWDNPKSLOQCCLTLR--TEGKEPDPPLYKTLQTVGFSHARTY	1298
293	FIRIVCFRLKHFIETSEKNWDKASHLQOWCLAMRDPSSSPDMPYKVLGIEGPTNNRIF	352
1299	TVAVYFKERIGCGKGPSIOQAEMGA---AMDALKENYFPQM-AHKRFPIGRKYQSELKE	1354
353	KIAYYTKRGLSAAESNVHKAELRVAELALANLESMSFKMKAKNNSNRRLEQDTS	412

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RESULT 4
US-09-513-990C-4635
; Sequence 4635, Application US/09513990C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

```

	Query Match	6.6%	Score 496;	DB 2;	Length 115;
	Best Local Similarity	95.7%;	Pred. No. 2.2e-31;		
	Matches 88;	Conservative 2;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	511	KKAHPRLHDLWYNPQGNNDGPKCSAKARRTGIRHSIYFGEEAIKCRPMTNNA	GR	570	
		:			
Db	24	KRXNLDRLHDLWYNPQGNNDGPKCSAKARRTGIRHSIYFGEEAIKCRPMTNNA	GR	83	
		:			
Qy	571	LFHYRITVSPPTNFLTDRPTVYDDHDEYIFE	602		
Db	84	LFHYRITVSPPTNFLTDRPTVYDDHDEYIFE	115		

```

RESULT 5
US-09-949-016-7961
; Sequence 7961, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7961
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7961

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Query Match 4.2%; Score 316; DB 2; Length 553;
Best Local Similarity 28.0%; Pred. No. 3.2e-16;
Matches 111; Conservative 32; Mismatches 106; Indels 148; Gaps 21;

[illegible]

RESULT 6
 US-09-107-532A-5434
 ; Sequence 5434, Application US/09107532A
 ; Patent No. 6583275
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 ;
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 ;
 ; NUMBER OF SEQUENCES: 7310
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street
 ; CITY: Waltham
 ; STATE: Massachusetts
 ; COUNTRY: USA

ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5434:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...241
SEQUENCE DESCRIPTION: SEQ ID NO: 5434:
US-09-107-532A-5434
Query Match 4.2%; Score 312.5; DB 2; Length 241;
Best Local Similarity 33.5%; Pred. No. 1.8e-16;
Matches 77; Conservative 50; Mismatches 90; Indels 13; Gaps 7;
QY 1105 OKLTEPEEAIGVIFTHVRLARAFTRTVGFNHH--LTIGHNORMEFLGDSIMOLVATEYL 1162
DB 17 QLTKEKENYNIIVFDNLNLEQAFTHSSVYNEHNLQSDNERLEFLGDAVLELWVSQYL 76
QY 1163 FIHPDHHGLTLRLSSLVNNRTQAKVAELGMQBYAITNDKTRPVGLRTK--TLADL 1220
DB 77 FLRYPHLPEGLTKTKRAAIVREDSLSKFAKECHFDQVLLIG-KGEENSGGRTPALLCDL 135
QY 1221 LESFIAALYTDKOLEYVHTFMNVCFPPRLKEFILNQDNDPKSQLQCCCLTLRTEGKEPD 1280
DB 136 FEAFGLGALYLDQGFDTTHAFIEKVIIPKVKAGAFSHEM-DHKTQLQE---VLQKSG---D 188
QY 1281 IPL-YKTLQTVGPSHARTYTVAVYFKGERIGCGKPSIQOAEANGAAMDAL 1329
DB 189 VSIEYRLNEEGPAHERVFIWVYVDDQLIGTGQGSKKLAEQAAENAL 238
RESULT 7
US-09-583-110-4554
Sequence 4554, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 4554
LENGTH: 232
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-583-110-4554
Query Match 3.8%; Score 284.5; DB 2; Length 232;
Best Local Similarity 32.9%; Pred. No. 2.8e-14;
Matches 76; Conservative 48; Mismatches 90; Indels 17; Gaps 8;
QY 1108 TEFEEAIGVIFTHVRLARAFTRTVGFNHH--LTIGHNORMEFLGDSIMOLVATEYLFTH 1165
DB 6 TVLKNHFAIEFTDKKLETAFTHTSYANEHRLKLSHNERLEFLGDAVLIQLISEVLYKK 65
QY 1166 FPDHHEGLTLRLSSLVNNRTQAKVAELGMQBYAITNDKTRPVGLRTK--TLADLLES 1223
DB 66 YPKPEGLDKLRAMIVREESLAGPARDCQDFQF-IKLGKGEKSGGRNRDITLGDAPFA 124
QY 1224 FTAALYTDKOLEYVHTFMNVCFPPRLK--EFLNQDNDPKSQLQCCCLTLRTEGKEPD 1281
DB 125 FLGALLLDKQVAKVKEFYQVMIPKVEAGSFEWITDY---KTHLQE---LLQVNG---DV 175
QY 1282 PL-YKTLQTVGPSHARTYTVAVYFKGERIGCGKPSIQOAEANGAAMDAL 1331
DB 176 AIRYQVISETGPADKVPDVEVLVEGKSGQCGKSKLAEQAAENAVEX 226
RESULT 8
US-09-107-433-4394
Sequence 4394, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4394:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES

```
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...236
; SEQUENCE DESCRIPTION: SEQ ID NO: 4394:
US-09-107-433-4394

Query Match
Best Local Similarity 3.8%; Score 284.5; DB 2; Length 236;
Matches 76; Conservative 48; Mismatches 90; Indels 17; Gaps 8;

Qy 1108 TEPEEAGVIVTHVRLARARLTATVGFNH--LTIGHNQMEFLGDSIMOLVATEYLPIH 1165
Db 10 TVLNKHPAIEFTDKLLETAPTHTSYANEHRLKISHNERLEFLGDAVLQLLSEYLYKK 69

Qy 1166 FPDHHEGLTLRLSSLVNNTQAKVBELOQVEYAITNDKTRPVGLRTK--TLADLLES 1223
Db 70 YPKKPEGDLKLRAMIVREESLAGPARDQDPQF--IKLGKEEKSQGNEDTILGDAFEA 128

Qy 1224 FIAALYTDKOLEVYHTPMNVCFPPRLK--BFILNQMDNPKSOLQCCCLTLRTGKBPDI 1281
Db 129 FLGALLLDKDVAKVEFIYQWMPKVEAGFEMITDY---KTHLQE---LLQVNG---DV 179

Qy 1282 PL-YKTLQTVGPHARYTYTAVYFKGERICGCKGPSIQQAEMGAMDALEK 1331
Db 180 AIRYQVISETPAHDKVFDEVLVEGKSIGQGGRSKGLAEQAAKNAVEK 230

RESULT 9
US-09-949-016-7757
; Sequence 7757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7757
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7757

Query Match
Best Local Similarity 3.8%; Score 284.5; DB 2; Length 998;
Matches 151; Conservative 63; Mismatches 206; Indels 245; Gaps 30;

Qy 27 ARPSA--PSRPNQLRLHQQBPVQVQYEPSSA-----PSTTFNSPAPNLP 75
Db 350 ARPGGGRPGWEHNS-KLGYLVSPQQIRRGERSCYRSINGRHHSERSQRTQGPS-LPAT 407

Qy 76 PDFVPPPPPPPSAQQGLPCCPIRPPPPNQHRRHPPVPPCPFPMPMPMPCNNPPVPGA 135
Db 408 PVFVPPPPP-----PLYPPPP-----HTLPLP---PGVPPQPSQPP--PGQ 445

Qy 136 PPGGTGTFPPMPPSPHPPPPPPVMPQQVN-----YQYPP----- 170
Db 446 PPPGPGF--YGVPPGPGF--PAPANLSTPWSSGVQTAHSNTIPTTQAPLRSREFFYRQR 501

Qy 171 -----GYSHHNPPPSFNS 184
Db 502 LKBEKKKSKLDFTNDFAKELMEYKIKQERRRSFSRSKSPYSGSSYSRSSTYKSGRS 561
```

```
Qy 185 FQNPSSFLPSANNSSPHRHLPPYPLPKAPSRERSPERLKYDHRHDSHGGERH 244
Db 562 GSTRSRYSRFSRSHSRYSRSPYP-----RRGRGKSRNY---RSRSRSHG---YH 608
Qy 245 RSLDRERGRSPDRRRQDSRYSDYD-RGRTPSRHRSYRSRER----- 289
Db 609 RS-----RSRSPYRYHRSRSPQAFRGQSPKRNVPQGETREYFNRYREVPYDMK 663
Qy 290 -----ERHRDNRSPSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPG 336
Db 664 AVYGRSVDPRDPPEKERYE-----WERKYREWEYKYYKGAAGAPRPSA----- 709
Qy 337 IINKTUSWAP-----PLEIVNHRSPSREKKARWESEKDRWSDNQSSG-----KD 381
Db 710 ---NRENFSRERFLPLNIRN--SPFTRGRREDTVGGSHRSRIGSNYPKLSARDGHNQ 764
Qy 382 KNYTSIKEPEPTMPD-----KNEEBEELKPVWIRCTH-----SENY 421
Db 765 KONTKSEKESENAPGDGKGNKHKKRRKKGESGFLNPELLETSRKSRPTGVEENK 824
Qy 422 YSS-----DPMQVGDSTVVTSLRLDLVDKFEEL-----GSRQ 456
Db 825 TDSLFLVPSRDDATPVDRDEMD--AESITFKSVSEKDKRERDKPAKGDKTKRKNDSAV 882
Qy 457 EKAKAARPWEPPKTKLDDLESSSESEC-----ESDEDSTCSSSSDSEVEDVIAEK 509
Db 883 SKKENTVTKPAKGQEKVDGERERSRSEPPKIKAKEETPKTNDTKSSSSQDEKITGTP 942

510 RKAH 514
943 R-KAH 946

RESULT 10
US-08-869-674-2
; Sequence 2, Application US/08869674
; Patent No. 5866365
; GENERAL INFORMATION:
; APPLICANT: Lonetto, Michael A.
; APPLICANT: Rosenberg, Martin
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,674
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: GM10013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
```

QY	1108	TEFEAIGVIFTHVRLARAFTRLRTVGFNH--LTLGHNQRMFEFGDSIMOLVATEYLFH	1165
DB	6	TVLKNHFAIEFADKNLLETAFTHTSYANEHRLLIKISHNERLEFLGDAVLQLLISEYLYKK	65
QY	1166	FPDHHEGHLTLRSSLVNNRTOAKVAEELGMOEYAITNDKTRPVGLRTK--TLADLLES	1223
DB	66	YPKPEGDLKSLRAMIVREESLAGFARDQDF--IKLKGEEKSGGRNDRDTILGDAFEA	124
QY	1224	FTAALYTDKOLEYVHTFMNVCFPPRLK--EFILNQDNNDPKSQLOQCCLTLRTGKEPDI	1281
DB	125	FLGALLLDKDAKVEFIYQVMPKVEAGEFEMITDY---KTHLQE---LLQVNG---DV	175
QY	1282	PL-YKTLOTGVPSSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDALK	1331
DB	176	AIRYQVISETPAHDKVDFVEVLVEGKSGIGGQGRSKKLAEQAANKNAVEK	226
RESULT 12			
US-09-213-011-2			
; Sequence 2, Application US/09213011			
; Patent No. 6444208			
; GENERAL INFORMATION:			
; APPLICANT: Lonetto, Michael A.			
; APPLICANT: Rosenberg, Martin			
; TITLE OF INVENTION: NOVEL COMPOUNDS			
; NUMBER OF SEQUENCES: 4			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Dechert Price & Rhoads			
; STREET: 997 Lenox Drive, Building 3, Suite 210			
; CITY: Lawrenceville			
; STATE: NJ			
; COUNTRY: USA			
; ZIP: 08543			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: DOS			
; SOFTWARE: FastSEQ for Windows Version 2.0			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/213,011			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/869,674			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Bloom, Allen			
; REGISTRATION NUMBER: 29,135			
; REFERENCE/DOCKET NUMBER: GM10013			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 609-520-3214			
; TELEFAX: 609-520-3259			
; TELEX:			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 232 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
US-09-213-011-2			
Query Match 3.7%; Score 277.5; DB 2; Length 232;			
Best Local Similarity 32.5%; Pred. No. 9.8e-14;			
Matches 75; Conservative 47; Mismatches 92; Indels 17; Gaps 8;			
QY	1108	TEFEAIGVIFTHVRLARAFTRLRTVGFNH--LTLGHNQRMFEFGDSIMOLVATEYLFH	1165
DB	6	TVLKNHFAIEFADKNLLETAFTHTSYANEHRLLIKISHNERLEFLGDAVLQLLISEYLYKK	65
QY	1166	FPDHHEGHLTLRSSLVNNRTOAKVAEELGMOEYAITNDKTRPVGLRTK--TLADLLES	1223
DB	66	YPKPEGDLKSLRAMIVREESLAGFARDQDF--IKLKGEEKSGGRNDRDTILGDAFEA	124
QY	1224	FTAALYTDKOLEYVHTFMNVCFPPRLK--EFILNQDNNDPKSQLOQCCLTLRTGKEPDI	1281
DB	125	FLGALLLDKDAKVEFIYQVMPKVEAGEFEMITDY---KTHLQE---LLQVNG---DV	175
QY	1282	PL-YKTLOTGVPSSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDALK	1331
DB	176	AIRYQVISETPAHDKVDFVEVLVEGKSGIGGQGRSKKLAEQAANKNAVEK	226
RESULT 11			
US-09-213-010-2			
; Sequence 2, Application US/09213010			
; Patent No. 6251630			
; GENERAL INFORMATION:			
; APPLICANT: Lonetto, Michael A.			
; APPLICANT: Rosenberg, Martin			
; TITLE OF INVENTION: NOVEL COMPOUNDS			
; NUMBER OF SEQUENCES: 4			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Dechert Price & Rhoads			
; STREET: 997 Lenox Drive, Building 3, Suite 210			
; CITY: Lawrenceville			
; STATE: NJ			
; COUNTRY: USA			
; ZIP: 08543			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: DOS			
; SOFTWARE: FastSEQ for Windows Version 2.0			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/213,010			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/869,674			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Bloom, Allen			
; REGISTRATION NUMBER: 29,135			
; REFERENCE/DOCKET NUMBER: GM10013			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 609-520-3214			
; TELEFAX: 609-520-3259			
; TELEX:			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 232 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
US-09-213-010-2			
Query Match 3.7%; Score 277.5; DB 2; Length 232;			
Best Local Similarity 32.5%; Pred. No. 9.8e-14;			
Matches 75; Conservative 47; Mismatches 92; Indels 17; Gaps 8;			

Qy	1224	PIAALYTDKOLEYYHTFMVNCFFPRLLK---EFILNQDWNDDPKSQLOQCCLLTURTEKEGPD	1281
Db	125	FLGALLDDKVAKYKBTIYQVMIPKVSAGEPEMITDY---KTHLQE---LLQVNG---DV	175
Qy	1282	PL-YKTLQTGVGSHARYTTVAVYKGERIGCGKGPSIQQAEWGMAADALEK	1331
Db	176	AIRYGVTSSETGFADKHVDVEVLVEGKSIIGOGQGRSKKLAEQEAANKVAEK	226

RESULT 13

```

RESUMI 13
US-09-461-774-10
; Sequence 10, Application US/09461774
; Patent No. 6987481
; GENERAL INFORMATION:
; APPLICANT: CHAN, Lily
; APPLICANT: CHUNG, Maxey Ching Ming
; APPLICANT: LIM, Renee Lay Hong
; TITLE OF INVENTION: Bacterial-deriv
; TITLE OF INVENTION: diagnostic uses
; FILE REFERENCE: 1781-0180P
; CURRENT APPLICATION NUMBER: US/09/4
; CURRENT FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 386
; TYPE: PR1
; ORGANISM: Mycobacterium tuberculosis
US-09-461-774-10

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Query Match 3.6%; Score 271.5; DB 2; Length 386;
Best Local Similarity 35.4%; Pred. No. 6.1e-13;
Matches 80; Conservative 9; Mismatches 88; Indels 49; Gaps 11;

[illegible]

RESULT 14

```

RESULI 14
US-08-365-087-2
; Sequence 2, Application US/08965087
; Patent No. 6346393
; GENERAL INFORMATION:
; APPLICANT: Pedon, Jason C.
; APPLICANT: Lonetto, Michael A.
; APPLICANT: Marra, Andrea
; APPLICANT: Palmer, Leslie M.
; APPLICANT: Rosenberg, Martin
; APPLICANT: Warren, Richard L.
; TITLE OF INVENTION: NOVEL RUCS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:

```

```

, MEDIUM TYPE: Diskette
, COMPUTER: IBM Compatible
, OPERATING SYSTEM: DOS
, SOFTWARE: FastSeq for Windows Version 2.0
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/965,087
, FILING DATE:
, CLASSIFICATION: 435
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER:
, FILING DATE:
, ATTORNEY/AGENT INFORMATION:
, NAME: Dickinson, Todd Q
, REGISTRATION NUMBER: 28,354
, REFERENCE/DOCKET NUMBER: GM10116
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 215-994-2252
, TELEFAX: 215-994-2222
, TELEX:
, INFORMATION FOR SEQ ID NO: 2:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 243 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, US-08-965-087-2

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Query Match 3.6%; Score 267; DB 2; Length 243;
Best Local Similarity 30.5%; Pred. No. 7e-13;
Matches 75: Conservative 55; Mismatches 92; Indels 24; Gaps 9;

[illegible]

RESULT 15

RESULT 15
 US-08-801-308-1
 ; Sequence 1, Application US/08801308
 ; Patent No. 6368790
 ; GENERAL INFORMATION:
 ; APPLICANT: Scott, Robert E.
 ; TITLE OF INVENTION: CDNA ENCODING P2P PROTEINS AND USE OF
 ; TITLE OF INVENTION: P2P CDNA-DERIVED ANTIBODIES AND ANTITENSE REAGENTS IN
 ; TITLE OF INVENTION: DETERMINING THE PROLIFERATIVE POTENTIAL OF NORMAL,
 ; TITLE OF INVENTION: ABNORMAL AND CANCER CELLS IN ANIMALS AND HUMANS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Weiser & Associates, P.C.
 ; STREET: 230 S. Fifteenth Street, Suite 500
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/801,308
;   FILING DATE: 18-FEB-1997
;   CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Weiser, Gerard J.
;     REGISTRATION NUMBER: 19,763
;     REFERENCE/DOCKET NUMBER: 372.6435P
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 215-875-8383
;       TELEFAX: 215-875-8394
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1404 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;   US-08-801-308-1

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Query Match 3.5%; Score 264.5; DB 2; Length 1404;
Best Local Similarity 19.9%; Pred. NO. 1.4e-11;
Matches 214; Conservative 125; Mismatches 327; Indels 411; Gaps 50;

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QY 134 GAPPQGGT--FPMPMPSPMPHPPPPVMPQVNYQ---YPPGY--SHNFPPPS----- 181
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Db 663 RGRREDYACQSHRNRLGNYPEKLSTRSHNAKNPKSKESSENVPGDGGKHKKH 722
QY 399 ---KNE-----EBEELKXVMI---RC-----THSENY---SSDPMQVGDSTVVG 437
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QY 438 TS-RLRLDYDKFREEL-----GSRQEKAKAARPPWPPTKLDLEDLESS 481
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Search completed: December 24, 2005, 00:59:36
Job time : 55 secs

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QY 715 -----PEEIANMLQ-----WEELEWQYABECK-----GMIV 742
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QY 801 RHLL-----ANSPKVQKQTDKQKLAQREBEALOKIRQKNTMRREVTVVE-LSSQGFWKT 850
Db 1174 QHELRSKSGSASSEKGRAKDREHSGSEKDNPDKRKSGAQPDKESTVDRLUSEQGHFKT 1230

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 24, 2005, 00:51:20 ; Search time 190 Seconds
(without alignments)
3021.566 Million cell updates/sec

Title: US-10-774-974-2

Perfect score: 7500

Sequence: 1 MMQGNCHRMSPHGRGCRP.....MRWERHQREDEYEDIKK 1374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7500	100.0	1374	3	US-09-900-425A-2
2	7500	100.0	1374	4	US-10-079-185-2
3	7500	100.0	1374	4	US-10-774-974-2
4	7500	100.0	1374	4	US-10-805-919-2
5	7500	100.0	1374	6	US-11-001-993-2
6	7486	99.8	1374	5	US-10-723-860-281
7	7486	99.8	1374	5	US-10-756-149-4809
8	2963	39.5	1327	6	US-11-097-143-2409
9	2847	38.0	541	4	US-10-205-331-116
10	2463	32.8	466	4	US-10-774-974-37
11	1961	26.1	378	4	US-10-103-313-471
12	1320	17.6	263	4	US-10-103-313-307
13	890	11.9	412	3	US-09-900-425A-3
14	890	11.9	412	4	US-10-079-185-3
15	890	11.9	412	4	US-10-774-974-3
16	890	11.9	412	4	US-10-805-919-3
17	890	11.9	412	6	US-11-001-993-3
18	340	4.5	1151	6	US-11-097-143-11586
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21	303.5	4.0	406	5	US-10-450-763-57609
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26	285.5	3.8	258	4	US-10-437-963-159481
27	284.5	3.8	236	5	US-10-617-320-4394

28	284.5	3.8	1616	5	US-10-934-998-88	Sequence 88, Appl
29	282.5	3.8	445	4	US-10-437-963-161789	Sequence 161789,
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32	280	3.7	266	4	US-10-425-115-189501	Sequence 189501,
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39	276	3.7	948	4	US-10-308-448-15	Sequence 15, Appl
40	276	3.7	948	5	US-10-934-998-295	Sequence 295, App
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45	273.5	3.6	431	4	US-10-437-963-204963	Sequence 204963,

ALIGNMENTS

RESULT 1

US-09-900-425A-2
; Sequence 2, Application US/09900425A
; Patent No. US20020164601A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Hongjiang
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Human RNase III and Compositions and Uses Thereof
; FILE REFERENCE: ISPH-0522
; CURRENT APPLICATION NUMBER: US/09/900,425A
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US 09/479,783
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 08/870,608
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 80/659,440
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-900-425A-2

Query Match	100.0%;	Score	7500;	DB	3;	Length	1374;
Best Local Similarity	100.0%;	Pred. No.	0;				
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Gaps	0;						
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QY	61	TTFSNSPAFNLPDPDFVPPPPMPPSAQGLP	PCPIRPPFNHQRHFPVPPPCFPPM	120			
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QY	121	PPMPCNNPPVPGAPGGGTFFMMPPSPMHP	PPPPVPMQVQYPPGYSHNPPPP	180			
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Db 361 KXARWEEKDRWSDNOSGKDKNYTSIKKEPBTMPDKNEEBELLKPVMIRCTHSEN 420
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US-10-079-185-2
; Sequence 2, Application US/10079185
; Publication No. US20030044941A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof
; FILE REFERENCE: ISIS5030
; CURRENT APPLICATION NUMBER: US/10/079,185
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 09/479,783
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 08/870,608
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 08/659,440
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 09/900,425
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1374
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-079-185-2

Query Match 100.0%; Score 7500; DB 4; Length 1374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3

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US-10-774-974-2
; Sequence 2, Application US/10774974
; Publication No. US20040126867A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof
; FILE REFERENCE: ISIS029/ISPH-0522
; CURRENT APPLICATION NUMBER: US/10/774, 974
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: US/09/900, 425B
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-774-974-2
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Query Match 100.0%; Score 7500; DB 4; Length 1374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MMOGNTCHRMSPFHPGRGCPGRGCHGARSAPSFRQNLLELHPQQPVQYQYEPSPAPS 60
QY 61 TTFSPNAPDNFLPRPDPFVFPFPPMPSPSAQGLPPCPPIRPPFNFHQRHPPFPPPCPPPM 120
Db 61 TTFSPNAPDNFLPRPDPFVFPFPPMPSPSAQGLPPCPPIRPPFNFHQRHPPFPPPCPPPM 120
QY 121 PPMPCNNPPVPFAGPGGQTFPFMMPPSPMPPHPPPPVMPQVNYQYPPGYSHNPPPP 180
Db 121 PPMPCNNPPVPFAGPGGQTFPFMMPPSPMPPHPPPPVMPQVNYQYPPGYSHNPPPP 180
QY 181 SFNSFQNNPSSFLPSANNSSPHFRHLPPYPLPKAPSERPSPERLKHYYDDHRRHDSHGR 240
Db 181 SFNSFQNNPSSFLPSANNSSPHFRHLPPYPLPKAPSERPSPERLKHYYDDHRRHDSHGR 240
QY 241 GERHSLDRRERGRSPDRRRQDSRYRSDYDRGRTPSRHRYSYRERERERHRHRDNRRS 300
Db 241 GERHSLDRRERGRSPDRRRQDSRYRSDYDRGRTPSRHRYSYRERERERHRHRDNRRS 300
QY 301 PSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEBIIKNVDSWAPPLEIVNHRSPREK 360
Db 301 PSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEBIIKNVDSWAPPLEIVNHRSPREK 360
QY 361 KRARWEEBKDRWSDNOSGDKNYTTSIKESPEBTMPDKNEEEEBELLKPVWIRCTHSEN 420
Db 361 KRARWEEBKDRWSDNOSGDKNYTTSIKESPEBTMPDKNEEEEBELLKPVWIRCTHSEN 420
QY 421 YTSDDPMDQVGDSTVVTGTSRLDLYDKFBEELSGROBKAKAAPPPWEPPTKLDDELESS 480
Db 421 YTSDDPMDQVGDSTVVTGTSRLDLYDKFBEELSGROBKAKAAPPPWEPPTKLDDELESS 480
QY 481 SESECSDESDSTCSSSDSEVFDVIAIKRKAHPDLRDLHDELWYNDPQGMNDGPLCKCSA 540
Db 481 SESECSDESDSTCSSSDSEVFDVIAIKRKAHPDLRDLHDELWYNDPQGMNDGPLCKCSA 540
QY 541 KARTGIRHSIYPGEBAIKPCRPMTNAGRLFHYRITVSPPTNFLTDRPTVIBYDDHEIYI 600
Db 541 KARTGIRHSIYPGEBAIKPCRPMTNAGRLFHYRITVSPPTNFLTDRPTVIBYDDHEIYI 600
QY 601 FEGFSMFAHAPLTNIPLCKVIRENIDYTHFIEBEMMPENFCVKGLEFLFLFRDILELY 660
Db 601 FEGFSMFAHAPLTNIPLCKVIRENIDYTHFIEBEMMPENFCVKGLEFLFLFRDILELY 660
QY 661 DWNKGLPFDSPCCPRFHFMPFRFVRFLPDGKEVLSMHQIILLYLLRCSKALVPBEEIA 720
Db 661 DWNKGLPFDSPCCPRFHFMPFRFVRFLPDGKEVLSMHQIILLYLLRCSKALVPBEEIA 720
QY 721 NMLQWEELEWQKVAECKGMIVTNPGTKPSSVRIDQLDREQFNPDIITPPIIVHFGIRPA 780
Db 721 NMLQWEELEWQKVAECKGMIVTNPGTKPSSVRIDQLDREQFNPDIITPPIIVHFGIRPA 780
QY 781 QLSYAGDPOYQKLWKSIVKLRHLLANSVKVQTDKQKLAQREBALOKIROKNTMRREVTV 840
Db 781 QLSYAGDPOYQKLWKSIVKLRHLLANSVKVQTDKQKLAQREBALOKIROKNTMRREVTV 840
QY 841 ELSQGFMTKGIKSDVCOHAMMLPVLTTHIRYHQCMLHLDKLGITFQDRCLLQALWTHP 900
Db 841 ELSQGFMTKGIKSDVCOHAMMLPVLTTHIRYHQCMLHLDKLGITFQDRCLLQALWTHP 900
QY 901 SHLNFQMPDHARNSLNSGIRQPKYGRKRVHMMMRKKGINTLINIMSRGQDDPTPS 960
Db 901 SHLNFQMPDHARNSLNSGIRQPKYGRKRVHMMMRKKGINTLINIMSRGQDDPTPS 960
QY 961 RINHNERLEFLGDVAVVEFLTSTVHLYYLFPSSLEGGGLATYRTAIVQNHLLAMAKKLELDP 1020
Db 961 RINHNERLEFLGDVAVVEFLTSTVHLYYLFPSSLEGGGLATYRTAIVQNHLLAMAKKLELDP 1020
QY 1021 FMYAHGPDLCRESDLRHAMANCFEALIGAVYLEGSLEEAQKQFGRLLFNDPDLREVWLN 1080
Db 1021 FMYAHGPDLCRESDLRHAMANCFEALIGAVYLEGSLEEAQKQFGRLLFNDPDLREVWLN 1080
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QY 1081 YLPHLQLOEPNTDRQLIETSPVLOKLTFFEEAIGVIFTHVRLARAFALTRTVGFNHLTL 1140
Db 1081 YLPHLQLOEPNTDRQLIETSPVLOKLTFFEEAIGVIFTHVRLARAFALTRTVGFNHLTL 1140
QY 1141 GHNQMEFLGDSIMQLVATEYLBIHPDPDHHEGLTLRLSSLVNNTQAKVABELGMOEYA 1200
Db 1141 GHNQMEFLGDSIMQLVATEYLBIHPDPDHHEGLTLRLSSLVNNTQAKVABELGMOEYA 1200
QY 1201 ITNDTKRPVGLRTKTLADLLESFIAALYTDKLEYVHTFMNVCFPPRLKEFTLNQDWND 1260
Db 1201 ITNDTKRPVGLRTKTLADLLESFIAALYTDKLEYVHTFMNVCFPPRLKEFTLNQDWND 1260
QY 1261 PKSLOQCCCLTLRTEGKEPDIPLYKLTQTVGSPHARTYTVAVYFKGERICGKGPSIQQA 1320
Db 1261 PKSLOQCCCLTLRTEGKEPDIPLYKLTQTVGSPHARTYTVAVYFKGERICGKGPSIQQA 1320
QY 1321 EMGAAMDALEKYNFPQMAHQKRFGRKYRQELKEMWREHQBREPDETDIKK 1374
Db 1321 EMGAAMDALEKYNFPQMAHQKRFGRKYRQELKEMWREHQBREPDETDIKK 1374

RESULT 4
US-10-805-919-2
; Sequence 2, Application US/10805919
; Publication No. US20040175828A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Human RNase III and Compositions and Uses Thereof
; FILE REFERENCE: ISPH-0522
; CURRENT APPLICATION NUMBER: US/10/805,919
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US/09/900,425
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 09/479,783
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 08/870,608
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: US 80/659,440
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-805-919-2

Query Match 100.0%; Score 7500; DB 4; Length 1374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMQGNTRCHMSFHPGRGCRGGRGHGARGSPAFRPNQLRLHPQQPPVQYQYPPSAPS 60
Db 1 MMQGNTRCHMSFHPGRGCRGGRGHGARGSPAFRPNQLRLHPQQPPVQYQYPPSAPS 60
QY 61 TTFNSPAPNLFPRDFVFPFPPMPPSAQGLPPCPPIRPPFPHQMRHPFPVPPCFPPM 120
Db 61 TTFNSPAPNLFPRDFVFPFPPMPPSAQGLPPCPPIRPPFPHQMRHPFPVPPCFPPM 120
QY 121 PPMPCPNPPVPGAPPGQGTFFPMPMPSPSMHPPPPVPVMPQVNYQYPPGYSHNFPPP 180
Db 121 PPMPCPNPPVPGAPPGQGTFFPMPMPSPSMHPPPPVPVMPQVNYQYPPGYSHNFPPP 180
QY 181 SFNSFQNNPSSFLPSANNSSPHRLPPYPLPKAFSPERRSPERLKHDDHRRDHSGR 240
Db 181 SFNSFQNNPSSFLPSANNSSPHRLPPYPLPKAFSPERRSPERLKHDDHRRDHSGR 240
QY 241 GERHSLDRRERGRSDRRQRDSYDGRGTPSRHHSYERSRERERHRRNRSS 300
Db 241 GERHSLDRRERGRSDRRQRDSYDGRGTPSRHHSYERSRERERHRRNRSS 300
QY 301 PSLSRYKKEYKRSGRSYGLSVVPEPAGCTPELPGBIIKNTDSWAPPLEIVNHRSPSREK 360
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RESULT 5

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US-11-001-993-2
; Sequence 2, Application US/11001993
; Publication No. US20050159384A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof
; FILE REFERENCE: ISIS0003-104 (ISIS-5030US.D1)
; CURRENT APPLICATION NUMBER: US/11/001,993
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: 10/079,185
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 09/479,783
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 08/870,608
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 08/659,440
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 09/900,425
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 1374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-001-993-2

Query Match      100.0%; Score 7500; DB 6; Length 1374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMQGNCTHRMSFHPGRCGRGCHGARSAPSFRQNLRLHLPQPPVQYQVEPPSAPS 60
DB 1 MMQGNCTHRMSFHPGRCGRGCHGARSAPSFRQNLRLHLPQPPVQYQVEPPSAPS 60
QY 61 TTFNSPAPNELPPRDFVPEPPMPPSAQGLPPCPPIRPPPNHOMRHPFVPPPCFPPM 120
DB 61 TTFNSPAPNELPPRDFVPEPPMPPSAQGLPPCPPIRPPPNHOMRHPFVPPPCFPPM 120
QY 121 PPPMPCNNPPVPGAPPGQGTFFPMPPPPSMHPPPPPVMPQVQNYQYPGGYSHNFPFP 180
DB 121 PPPMPCNNPPVPGAPPGQGTFFPMPPPPSMHPPPPPVMPQVQNYQYPGGYSHNFPFP 180
QY 181 SFNSFQNNPSSFLPSANNSSPHRLPPYPLPKAPSERRSPRLKHYYDDHRRHDSHGR 240
DB 181 SFNSFQNNPSSFLPSANNSSPHRLPPYPLPKAPSERRSPRLKHYYDDHRRHDSHGR 240
QY 241 GERHSLDRRGRSPDRRQDSRYESDYDRGTPSRHSYSRERERERHRRHNRSS 300
DB 241 GERHSLDRRGRSPDRRQDSRYESDYDRGTPSRHSYSRERERERHRRHNRSS 300
QY 301 PSLSRYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIINKTDSWAPPLEIVNHRSPSREK 360
DB 301 PSLSRYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIINKTDSWAPPLEIVNHRSPSREK 360
QY 361 KQARWEEKDRWSDNOSGKDKNTYSIKKEPEETMPDKNEEBEELLKPWIRCTHSEN 420
DB 361 KQARWEEKDRWSDNOSGKDKNTYSIKKEPEETMPDKNEEBEELLKPWIRCTHSEN 420
QY 421 YVSSDPMQVGSSTVVGTSRLDLYDKPFEELGSRQEKAKAAPPPWEPKTKLDEDLSS 480
DB 421 YVSSDPMQVGSSTVVGTSRLDLYDKPFEELGSRQEKAKAAPPPWEPKTKLDEDLSS 480
QY 481 SESECESDSDTSCSSSDSEVFDTAIEIKKKAHPDLRLHDELWYNDPGQWMDGCLCKSA 540
DB 481 SESECESDSDTSCSSSDSEVFDTAIEIKKKAHPDLRLHDELWYNDPGQWMDGCLCKSA 540
QY 541 KARTGIRHSIYPGEBAIKPCPMTNNAAGLPHYRITVSPPTNFLTDRPTVIEYDDHEVI 600
DB 541 KARTGIRHSIYPGEBAIKPCPMTNNAAGLPHYRITVSPPTNFLTDRPTVIEYDDHEVI 600
QY 601 PEGFSMFAHAPLTNIPLCVKVIRENIDYTHFIEEMMPENFCVKGLELFLFLFRDILELY 660
DB 601 PEGFSMFAHAPLTNIPLCVKVIRENIDYTHFIEEMMPENFCVKGLELFLFLFRDILELY 660
QY 661 DWNLKGPLFEDSPCCPRFHFMPFRFVRFLPDGQKEVLSMHQIILLYLLRCSKALVPBEEIA 720
DB 661 DWNLKGPLFEDSPCCPRFHFMPFRFVRFLPDGQKEVLSMHQIILLYLLRCSKALVPBEEIA 720
QY 721 NMLQWEELEWQYABECKGMIVTNPGTKPSSSVRIDQLDRQFNPDVITTFPIIVHFGIRPA 780
DB 721 NMLQWEELEWQYABECKGMIVTNPGTKPSSSVRIDQLDRQFNPDVITTFPIIVHFGIRPA 780
QY 781 QLSYAGDPQYQKLMKSYVVKLRHLLANS PKVQTKDQKLAQREBALQKIROKNTMRREVTV 840
DB 781 QLSYAGDPQYQKLMKSYVVKLRHLLANS PKVQTKDQKLAQREBALQKIROKNTMRREVTV 840
QY 841 ELSQGFMTGIRSDVQCQHAMMLPVLTHIRYHQCILMHLDKLIGYTFQDRCLLQLANTHP 900
DB 841 ELSQGFMTGIRSDVQCQHAMMLPVLTHIRYHQCILMHLDKLIGYTFQDRCLLQLANTHP 900
QY 901 SHHLNFGMPPDHARNSLSNCGIRQPKYGDVKVHHMHRKKGINTLINIMSRLGQDDPTPS 960
DB 901 SHHLNFGMPPDHARNSLSNCGIRQPKYGDVKVHHMHRKKGINTLINIMSRLGQDDPTPS 960
QY 961 RINHNERLEFLGDVAVVEFLTSTVHLVYLPFSLBEGGLATYRTAIVQNHQHLAMAKLELDP 1020
DB 961 RINHNERLEFLGDVAVVEFLTSTVHLVYLPFSLBEGGLATYRTAIVQNHQHLAMAKLELDP 1020
QY 1021 FMLYAGHPDLCRESDLRHAMANCFEALIGAVYLEGSLEBAKQLFGRLLFNDPDLREVWLN 1080
DB 1021 FMLYAGHPDLCRESDLRHAMANCFEALIGAVYLEGSLEBAKQLFGRLLFNDPDLREVWLN 1080
QY 1081 YPLHPLQLOEPPNTDROLIETSPVLQKLTFFEEAIGVIFTHVRLARAFRTVTFGNHLLT 1140
DB 1081 YPLHPLQLOEPPNTDROLIETSPVLQKLTFFEEAIGVIFTHVRLARAFRTVTFGNHLLT 1140
QY 1141 GHNQRMFELGDSIMQLVATEYLFIFHPDHEHGLTLRLSSLVNNRTQAKVAEELGMOEYA 1200
DB 1141 GHNQRMFELGDSIMQLVATEYLFIFHPDHEHGLTLRLSSLVNNRTQAKVAEELGMOEYA 1200
QY 1201 ITNDTKRPVGLRTKTLADLLSFTAAALYTDKDLVYHVTFMNVCFPPRLKEFTLNQDND 1260
DB 1201 ITNDTKRPVGLRTKTLADLLSFTAAALYTDKDLVYHVTFMNVCFPPRLKEFTLNQDND 1260
QY 1261 PKSQLOOCCCLTARTEGKPDIPLYKTLQTVGSPHARTYTVAVYFKGERICGCGKPSIQQA 1320
DB 1261 PKSQLOOCCCLTARTEGKPDIPLYKTLQTVGSPHARTYTVAVYFKGERICGCGKPSIQQA 1320
QY 1321 EMGAAMDALCKYNFQMAHQKRFGRKYQELKEMWREHOREPDEDEDIKK 1374
DB 1321 EMGAAMDALCKYNFQMAHQKRFGRKYQELKEMWREHOREPDEDEDIKK 1374

RESULT 6
US-10-723-860-281
; Sequence 281, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 281
; LENGTH: 1374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-281
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Query Match		99.8%;	Score 7486;	DB 5;	Length 1374;	
Best Local Similarity		99.9%;	Pred. No. 0;			
Matches 1372;		Conservative	0;	Mismatches	2;	Indels 0; Gaps 0;
Qy	1	MMQGNCTCHRMSPHGRGCGRGGHGCARPSAFRPNQLRLHLPQPPVQYQVEPSPAPS	60			
Db	1	MMQGNCTCHRMSPHGRGCGRGGHGCARPSAFRPNQLRLHLPQPPVQYQVEPSPAPS	60			
Qy	61	TTFSNSPAPNLFPPRDFVFPFPPMPSPAGGLPPCPIRPPPNHOMRHPFPVPPCFPPM	120			
Db	61	TTFSNSPAPNLFPPRDFVFPFPPMPSPAGGLPPCPIRPPPNHOMRHPFPVPPCFPPM	120			
Qy	121	PPMPCPNPPVPGAPGGGTFFMMPPSPMHPPPPVMQOVNYQYPPGYSHHFPFP	180			
Db	121	PPMPCPNPPVPGAPGGGTFFMMPPSPMHPPPPVMQOVNYQYPPGYSHHFPFP	180			
Qy	181	SFNSFQNNPSSFLPSANNSSPHFRHLPPYPLPKAPSERSSPERLKHDDHRRDHSRGR	240			
Db	181	SFNSFQNNPSSFLPSANNSSPHFRHLPPYPLPKAPSERSSPERLKHDDHRRDHSRGR	240			
Qy	241	GERHSLDRRGRSPDRRRQDSRYSDYDRGTPSRHRSYERSRERERHRHRDNRRS	300			
Db	241	GERHSLDRRGRSPDRRRQDSRYSDYDRGTPSRHRSYERSRERERHRHRDNRRS	300			
Qy	301	PSLSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSPSREK	360			
Db	301	PSLSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSPSREK	360			
Qy	361	KXARWEEEDKRWSDNOSGKDKNYTSGIKEKEPETMPDKNEEBEELLKPVWIRCTHSEN	420			
Db	361	KXARWEEEDKRWSDNOSGKDKNYTSGIKEKEPETMPDKNEEBEELLKPVWIRCTHSEN	420			
Qy	421	YSSSDPMDQVGDSTVVGTSRLRLDLYDKFEEELSGRQEKAKAAPPPWEPKTKLDEDLSS	480			
Db	421	YSSSDPMDQVGDSTVVGTSRLRLDLYDKFEEELSGRQEKAKAAPPPWEPKTKLDEDLSS	480			
Qy	481	SESECESEDSTCSSSDSEVFVIAIEIKRKAHPDRLHDELWYNDPGQWMDGLCKCSA	540			
Db	481	SESECESEDSTCSSSDSEVFVIAIEIKRKAHPDRLHDELWYNDPGQWMDGLCKCSA	540			
Qy	541	KARRTGIRHSIYGEBAIKPCRMTNAGRLPHYRITVSPPTNFLTDRPTVITYDDHEVI	600			
Db	541	KARRTGIRHSIYGEBAIKPCRMTNAGRLPHYRITVSPPTNFLTDRPTVITYDDHEVI	600			
Qy	601	FEGFSMAFAHPLTNIPLCKVIRENIDYTHIFIEEMMPENFCVKGLELSLFLFRDILELY	660			
Db	601	FEGFSMAFAHPLTNIPLCKVIRENIDYTHIFIEEMMPENFCVKGLELSLFLFRDILELY	660			
Qy	661	DNMLKGPLFEDSPCCPRHFMPFRVFLPDGSGKEVLSMHQIILLYLLRCSKALVPEETA	720			
Db	661	DNMLKGPLFEDSPCCPRHFMPFRVFLPDGSGKEVLSMHQIILLYLLRCSKALVPEETA	720			
Qy	721	NMLQWELEWQKAECKGMIVNPGTKPSSVRIQDLDRQFNPDVITTPIIIVHFGIRPA	780			
Db	721	NMLQWELEWQKAECKGMIVNPGTKPSSVRIQDLDRQFNPDVITTPIIIVHFGIRPA	780			
Qy	781	QLSYAGDPQYQKLWKSYYKLRLHLLANSPKVKQTDKQLAQREBALQIKRQNTMRRETV	840			
Db	781	QLSYAGDPQYQKLWKSYYKLRLHLLANSPKVKQTDKQLAQREBALQIKRQNTMRRETV	840			
Qy	841	ELSSQGFWKTGIRSDVCQHMMPLVLTTHIRYHQLMHLDKLIGYTFQDRCLLQLANTHP	900			
Db	841	ELSSQGFWKTGIRSDVCQHMMPLVLTTHIRYHQLMHLDKLIGYTFQDRCLLQLANTHP	900			
Qy	901	SHHLNFGMNDHARNISLNCIGIQPKYGDGRKVHMMMRKKGINTLINIMSLRGQDDPTPS	960			
Db	901	SHHLNFGMNDHARNISLNCIGIQPKYGDGRKVHMMMRKKGINTLINIMSLRGQDDPTPS	960			
Qy	961	RINHNERLEFGDAVVEFLTSSVHLYYLFPSLEBGGATYRTAIVQNHAMLAUKLELDP	1020			
Db	961	RINHNERLEFGDAVVEFLTSSVHLYYLFPSLEBGGATYRTAIVQNHAMLAUKLELDP	1020			

Qy	1021	FMLYAHGPDLCRESDLRHAMANCFEALIGAVYLEGSLEBAKQFGRLLFNDPDLREVWLN	1080			
Db	1021	FMLYAHGPDLCRESDLRHAMANCFEALIGAVYLEGSLEBAKQFGRLLFNDPDLREVWLN	1080			
Qy	1081	YPLHPLQLOEPNTDQLIETSPVLOKLTBFEBEIGAIVIFTHVPLLLARAFPLRTVGFNHLTL	1140			
Db	1081	YPLHPLQLOEPNTDQLIETSPVLOKLTBFEBEIGAIVIFTHVPLLLARAFPLRTVGFNHLTL	1140			
Qy	1141	GHNORMEFLGDSIMQVATEYLFIFHPDHHGHGHTLLRSSLVNNRTQAAKVAEELGMOEYA	1200			
Db	1141	GHNORMEFLGDSIMQVATEYLFIFHPDHHGHGHTLLRSSLVNNRTQAAKVAEELGMOEYA	1200			
Qy	1201	ITNDTKRPVGLRTKTTLADLLESFIAALYTDKDLLEVHTFMNVCFPPRLKEFILNQDWND	1260			
Db	1201	ITNDTKRPVGLRTKTTLADLLESFIAALYTDKDLLEVHTFMNVCFPPRLKEFILNQDWND	1260			
Qy	1261	PKSQLOQCCLTLRTGKBPDIPLYKTLQTVGSPSHARTYTVAVYFKGERIGCGKGPSIOQA	1320			
Db	1261	PKSQLOQCCLTLRTGKBPDIPLYKTLQTVGSPSHARTYTVAVYFKGERIGCGKGPSIOQA	1320			
Qy	1321	EMGAAMDALKYNFQMAHOKBFIGRKYROELKEMWEREHOREBDEDEDIKK	1374			
Db	1321	EMGAAMDALKYNFQMAHOKBFIGRKYROELKEMWEREHOREBDEDEDIKK	1374			

RESULT 7

US-10-756-149-4809
; Sequence 4809, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4809
; LENGTH: 1374
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4809

Query Match 99.8%; Score 7486; DB 5; Length 1374;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1372; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MMQGNCTCHRMSPHGRGCGRGGHGCARPSAFRPNQLRLHLPQPPVQYQVEPSPAPS	60			
Db	1	MMQGNCTCHRMSPHGRGCGRGGHGCARPSAFRPNQLRLHLPQPPVQYQVEPSPAPS	60			
Qy	61	TTFSNSPAPNLFPPRDFVFPFPPMPSPAGGLPPCPIRPPPNHOMRHPFPVPPCFPPM	120			
Db	61	TTFSNSPAPNLFPPRDFVFPFPPMPSPAGGLPPCPIRPPPNHOMRHPFPVPPCFPPM	120			
Qy	121	PPMPCPNPPVPGAPGGGTFFMMPPSPMHPPPPVMQOVNYQYPPGYSHHFPFP	180			
Db	121	PPMPCPNPPVPGAPGGGTFFMMPPSPMHPPPPVMQOVNYQYPPGYSHHFPFP	180			
Qy	181	SFNSFQNNPSSFLPSANNSSPHFRHLPPYPLPKAPSERSSPERLKHDDHRRDHSRGR	240			
Db	181	SFNSFQNNPSSFLPSANNSSPHFRHLPPYPLPKAPSERSSPERLKHDDHRRDHSRGR	240			
Qy	241	GERHSLDRRGRSPDRRRQDSRYSDYDRGTPSRHRSYERSRERERHRHRDNRRS	300			
Db	241	GERHSLDRRGRSPDRRRQDSRYSDYDRGTPSRHRSYERSRERERHRHRDNRRS	300			
Qy	301	PSLSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSPSREK	360			
Db	301	PSLSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSPSREK	360			

361 KRARWEEKORWSDNOSGKDKNYTSIKEPEETMPDKNEEBEELLPVWIRCTHSEN 420
361 KRARWEEKORWSDNOSGKDKNYTSIKEPEETMPDKNEEBEELLPVWIRCTHSEN 420
421 YSSDPMDQVGDSTVVTGTSRLDLYDKFEEELSGRQEKAKAAPPPWEPKTKLDEDESS 480
421 YSSDPMDQVGDSTVVTGTSRLDLYDKFEEELSGRQEKAKAAPPPWEPKTKLDEDESS 480
481 SESECEDESDSTCSSSDSEVFVIAEIKRKAHPORLHDELWYNDPGQNDGPKCKSA 540
481 SESECEDESDSTCSSSDSEVFVIAEIKRKAHPORLHDELWYNDPGQNDGPKCKSA 540
541 KARTGIRUSIYGEEBAIKPCRMWNNAGLPHYRITVSPPTNFLTDRPTVIEYDDHEVI 600
541 KARTGIRUSIYGEEBAIKPCRMWNNAGLPHYRITVSPPTNFLTDRPTVIEYDDHEVI 600
601 FEGFSMAHAPLTNIPLCKVIRENIDYTHIFIEEMPPENFCVKGLBELFSLFRDILELY 660
601 FEGFSMAHAPLTNIPLCKVIRENIDYTHIFIEEMPPENFCVKGLBELFSLFRDILELY 660
661 DNNLKGPLFEDSPCCPRFHFMRFRVFLPDGKKEVLSMHQIILLYLRCSKALVPEEETA 720
661 DNNLKGPLFEDSPCCPRFHFMRFRVFLPDGKKEVLSMHQIILLYLRCSKALVPEEETA 720
721 NMLQWEELEWQKVAECKGMIVNPGTKPSSVRIDQLDRQFNPDVITPPIIVHFGIRPA 780
721 NMLQWEELEWQKVAECKGMIVNPGTKPSSVRIDQLDRQFNPDVITPPIIVHFGIRPA 780
781 QLSYAGDPQYQKLMKSVYKRLHLLANSVKVQKTDKQKLAQREBALQKIRQKNTMRREVTV 840
781 QLSYAGDPQYQKLMKSVYKRLHLLANSVKVQKTDKQKLAQREBALQKIRQKNTMRREVTV 840
841 ELSQSGFKTKGIRSDVCOHAMMLPVLTTHIRYHQCLMHLDKLIGYTFQDRCLLQALWTHP 900
841 ELSQSGFKTKGIRSDVCOHAMMLPVLTTHIRYHQCLMHLDKLIGYTFQDRCLLQALWTHP 900
901 SHHNLFGMPDHARNISLNGIRQPKYGVKQVHMHMRKKGINTLINIMSLRGQDDPTPS 960
901 SHHNLFGMPDHARNISLNGIRQPKYGVKQVHMHMRKKGINTLINIMSLRGQDDPTPS 960
961 RINHNERLEFLGDVAVFEFTSVHLYLFPSSLEGGGLATYRTAIVQOHLAMLAKELEDP 1020
961 RINHNERLEFLGDVAVFEFTSVHLYLFPSSLEGGGLATYRTAIVQOHLAMLAKELEDP 1020
1021 FMLYHAGPDLGRESDLRHAMANCEALIGAVYLEGSLEBAKQLFGRLLPNDPLREVWLN 1080
1021 FMLYHAGPDLGRESDLRHAMANCEALIGAVYLEGSLEBAKQLFGRLLPNDPLREVWLN 1080
1081 YPLHPLQLOQEPNTDROLIETSPVLQKLTPEEAIQVIFTHVRLARAFTLRTVGFNHLTL 1140
1081 YPLHPLQLOQEPNTDROLIETSPVLQKLTPEEAIQVIFTHVRLARAFTLRTVGFNHLTL 1140
1141 GHNMREFLGDSIMQLVATEYLFTHPDHHEGLTLRLSLVNNRTQAKVABELGMQEYA 1200
1141 GHNMREFLGDSIMQLVATEYLFTHPDHHEGLTLRLSLVNNRTQAKVABELGMQEYA 1200
1201 ITNDTKRPVGLRTKTLADLLESFIAALYTDKOLEYVHTFMVNCFFPRLKEFLINQDND 1260
1201 ITNDTKRPVGLRTKTLADLLESFIAALYTDKOLEYVHTFMVNCFFPRLKEFLINQDND 1260
1261 PKSQLQCCCLTLTEGKEPDIPLYKLTQVGPSHARTYTVAVYFKGERIGCGKGPSIOQA 1320
1261 PKSQLQCCCLTLTEGKEPDIPLYKLTQVGPSHARTYTVAVYFKGERIGCGKGPSIOQA 1320
1321 EMGAAMDALKYNFPQMAHQKRIKRYQELKEMEREBHOREDEDEDIKK 1374
1321 EMGAAMDALKYNFPQMAHQKRIKRYQELKEMEREBHOREDEDEDIKK 1374

RESULT 8

US-11-097-143-2409

; Sequence 2409, Application US/11097143

; Publication No. US2005020858A1

GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2409
; LENGTH: 1327
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-2409

Query Match 39.5%; Score 2963; DB 6; Length 1327;

Best Local Similarity 45.6%; Pred. No. 7.8e-173;

Matches 621; Conservative 213; Mismatches 327; Indels 200; Gaps 32;

QY 90 QGPLPCPTIRPPFNHQMHPFVPCFPFPPMPMPCPN-NPPVPCAP-----P 137
DB 3 QPLPLPPVQPA-----PPPPPPPEEDLSPPGVGVFPHSNYSNESHQ 46
QY 138 GQPTFPFMPPPSPMHPPPPPVMPQVNYQYPPGY-----SHNFPP 179
DB 47 SKSLDYVPEPAPYASS---VPSYDVPYQPPAYGEGVAYNEQAQYGGQSHVQYQY 103
QY 180 PSFNSQNNPSPGLPSANNSSPHFRLPPYPL---PKAPSRERSPERLKHVDDHHRD 235
DB 104 PA-----SGSFLYES-----YKYPDRYPAYSSNYRPPSERQ-----RYTS 139
QY 236 HSHGRCGERHSLDRRGRSPDRRRQDSYRSYDGRGTPSRHSYRSRERERERHR 295
DB 140 NSSSQGYHYP-----GYSSGR-----RYEQRHQ-----EHRQIDSYAHEPRGHY 183
QY 296 DNRSPSLERSYKCKYKRSRSGVGLSVVPACGTPELPGEIINKTDSMAPPLEIVNHS 355
DB 184 AHRQAGSORGY---YGSARN-----QVSDDYSPRGHERERN 219
QY 356 PSREKKRA--RWEEERKDR---WSDNQSGKDKNYTSIKEPEETMPDKNEEBEELK 409
DB 220 ETLEKTRAKPKVETERDRLLRQWCSNFC-----EKEDYVKKGNALSEADAPV 267
QY 410 PWWIRCTHSEYSSPDMQVGDSTVVTGTSRLDLYDKFEEELSGRQEKAKAAPPPWEP 469
DB 268 ESWVRSPAEIYYERTK---GENEVGRARLQKLTCLFDEELQRAKRVREKLPVYVPP 323
QY 470 KTKL-----DEDLSSSECEDESDSTCSSSDSEVFDV-----IABIKRKAH 514
DB 324 PRKARRRVCKHKHKEACSSSSDDDDDEDA-----FKIQQCCMEELSRKQV 373
QY 515 PDRLHDELWYNDPGQNDGPKCKSAKARRTGIRHSIYPGEEAIKPCRPMTNNAFLHY 574
DB 374 PQRVHADLWHDAGENNDGFLCCKSAKRRIGIRHGIYFGETGYKCLDPNNAAGLFLHY 433

Qy	575	RITVSPPTNFLTDRPTVIEYDDHYIIFEGSMFAHALPTNIPICKYRFINIDYTHIFEE	634
Db	434	RISISPTNFTKTPTTIIKDEHEFEGFSLSHVLSLDPCKVIRFINIETIYEE	493
Qy	635	MPNPNFCVKGELFSLFLDRILELYDWNILKGPL-----PDSPPCCPRFHFMRFRVFLP	690
Db	494	KMPNFTIHELDIFPKYLFHELLELVDFNLPNLPNPGNVEES---CPAFHFFRFRVDRLP	550
Qy	691	DGGKEVLSMHQILLYLLYLRCSKALVPBEEIANMLQWEELWQKYABECKGMIVTNPQKPS	750
Db	551	DNGKEVLAMVEVLYRLLDNSAQLVERQQLHLNQISOSEWQNYVDFIKGMLVTKPGYKPC	610
Qy	751	SVRIDOLDRQFNDV-----ITPFIIVHEGIRPAQLSVAGDPOYOKLWKSYYKLR	801
Db	611	SLRVDQJDRN--NSDLPECVDRTGISHPAIVFHGICHPOLSVAGNPEYOKANREYKYR	668
Qy	802	HLANSPKVQTDKQKLAQREEAQKIRQKNTWRREVTVELSSOGFWKKTGIRSDVCOHAM	861
Db	669	HLMANMSPKDFKDKLEEQRLOEMRTQGRMKRNTVAISSEGFYRTGIMCDVVQHAM	728
Qy	862	MLPVLTHIRYHQCIMHLDKLIQVTFQDRCLLQLAMTHPSHHLNFGMNPDPHARNSLSNCG	921
Db	729	LIPVLTHLRFHKSLLDLEESIGYRFRKRYLLQALATHPSYKENGYTNPDPHARNSLTNCG	788
Qy	922	IRQPKYGDVKVHMHMKKGINTLINTMSRLGQDDPTSPRINNNERLEFLGDVAVREFLTS	981
Db	789	IRQPEYGDVKIHYNWKTRKGINTLIVSIVMSRPGKEHETVSNITNERLEFLGDVAVREFLSS	848
Qy	982	VHLYLFPFLEEGGLATYRTAIVQNOHMLAKKLELDPFMLYAHGPDLCRESDLRHAMA	1041
Db	849	IHLFMPFLEEGGLATYRAAIVQNOHLALLAKKLQLEEFMLYAHGSDICHELELRHAMA	908
Qy	1042	NCFEALLGAVYLEGSLBEAKQLFGRLLP--NDPDLREVWLYNPLHPLQLOPNTDRQLIET	1100
Db	909	NCFEALMGALLDGGIIVADEVEFTDALFRQDEKLLSIWKNLPEHPLOEQEPFLGDRSCIDS	968
Qy	1101	SPVLQKLTPEEEAGVPTFVRLLARAFPTLRTVGFNHLTLGHORMEFLGDSIMQLVATE	1160
Db	969	YRVUKELTKEDSICIGFKHIRLLARAFTRDSIGFTHLTIGSNQRLEFLGDTVLQLICSE	1028
Qy	1161	YLFTHFPDHPHGHUTLRLSSLVNNRNTQAKVABELGMQSYAI--TNDKTRPVGLRKTTLAD	1219
Db	1029	YLYRHFPEHEGHLSLLRSSLVNNRNTQAVVCCDLLGMPKYAVYANPK----ADLKTKDRAD	1084
Qy	1220	LLESFIAALYTDKLEVYHTFMNVCFPRLKEFTLNQDNDPKSQOQCCLTLRT--EGKE	1278
Db	1085	LLEAFGLAYVDKGLLYCEQFCHVCLFPRQLQFLIMNQDNDPKSKLQOCCCLTUTMDGGE	1144
Qy	1279	PDIPLYKTLQTVGPSHARTTVAVYFKEGIRIGCGKPSIOQAEMGAAMDALKEYN--FPQ	1336
Db	1145	PDIPYKVVASGPTNTRVYKVAVYFRSKRLATSSGSSIOQAEMNAAKALENSRDLFPQ	1204
Qy	1337	MAHQQRIFGRKYQEL---KEMRWERBHQREPDETEDIKK	1374
Db	1205	LDHQKRVIAKSIKQGTGNELDNDSDRQHQE-----EKIKR	1239

RESULT 9

```

RESUMI 9
US-10-205-331-116
; Sequence 116, Application US/10205331
; Publication No. US2004058326A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brookesbank, Robert
; APPLICANT: Pinnock, Robert
;
; TITLE OF INVENTION: Identification a
;
; FILE REFERENCE: Wf-A-018199
;
; CURRENT APPLICATION NUMBER: US/10/20
;
; CURRENT FILING DATE: 2002-07-24
;
; PRIOR APPLICATION NUMBER: GB 0118354
;
; PRIOR FILING DATE: 2001-07-27
;

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; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 116
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative ribonuclease III
US-10-205-331-116

Query Match      38.0%; Score 2847; DB 4; Length 541;
Best Local Similarity 99.3%; Pred. No. 3.2e-166;
Matches 537; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      834 MRREVTVELSSQGFWKTGIRSDVCQHAMMLPVLTHIRYHQCLMHLDKLIGYTFQDRCLL 893
Db      1 MRREVTVELSSQGFWKTGIRSDVCQHAMMLPVLTHIRYHQCLMHLDKLIGYTFQDRCLL 60

Qy      894 QLAWTHPSHLNFGMPPDHARNSLNSCGIRQPKYGDGRKVHMHMRKKGINTLINIMSRLG 953
Db      61 QLAWTHPSHLNFGMPPDHARNSLNSCGIRQPKYGDGRKVHMHMRKKGINTLINIMSRLG 120

Qy      954 QDDPTSRINHNRLRLEPLGDAVVEFTLSVHLVYLFPSLEEGGLATYRTAIVQOHLAML 1013
Db      121 QDDPTSRINHNRLRLEPLGDAVVEFTLSVHLVYLFPSLEEGGLATYRTAIVQOHLAML 180

Qy      1014 KCLELDPFMLYAHGPDICRESDLRHAMANCEALIGAVYLEGSLAEAKQLFGRLLFNDPDP 1073
Db      181 KCLELDRFMLYAHGPDICRESDLRHAMANCEALIGAVYLEGSLAEAKQLFGRLLFNDPDP 240

Qy      1074 LREWLNYPHLPLQLOEPNTDROLIETSPVLQKLTFFEEAIGVIFTHVRLARAFTLRTV 1133
Db      241 LREWLNYPHLPLQLOEPNTDROLIETSPVLQKLTFFEEAIGVIFTHVRLARAFTLRTV 300

Qy      1134 GFNHLTIGHNORMEFLGDSIMQLVATEYLFHPDPDHHEGHLTLRLSSLVNNRTOAKVAEE 1193
Db      301 GFNHLTIGHNORMEFLGDSIMQLVATEYLFHPDPDHHEGHLTLRLSSLVNNRTOAKVAEE 360

Qy      1194 LGMQEVAITNDTKRPVGLTKTKTLADLLESFIAALYTDKOLEVYHTPMNVCFPPRLKEFI 1253
Db      361 LGMQEVAITNDTKRPVALRTKTKTLADLLESFIAALYTDKOLEVYHTPMNVCFPPRLKEFI 420

Qy      1254 LNQDWNPKSQLOCCCLTLTEGKEPDIPLYKTLQTVGPSHARTYTVAVYFKGERIGCGK 1313
Db      421 LNQDWNPKSQLOCCCLTLTEGKEPDIPLYKTLQTVGPSHARTYTVAVYFKGERIGCGK 480

Qy      1314 GPSIQQAEMGAAMDALSKYNFPQWAKRFGIRKYOELKMRWEREHOERPEDETDIK 1373
Db      481 GPSIQQAEMGAAMDALSKYNFPQWAKRFGIRKYOELKMRWEREHOERPEDETDIK 540

Qy      1374 K 1374
Db      541 K 541

RESULT 10
US-10-774-974-37
; Sequence 37, Application US/10774974
; Publication No. US20040126867A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof
; FILE REFERENCE: ISIS029/ISPH-0522
; CURRENT APPLICATION NUMBER: US/10/774,974
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: US/09/900,425B
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 37
; LENGTH: 466
; TYPE: PRT

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```
; ORGANISM: Homo sapiens
US-10-774-974-37

Query Match      32.8%; Score 2463; DB 4; Length 466;
Best Local Similarity 100.0%; Pred. No. 9.9e-143;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 909 NPDHARNSLNCGIROPKYGDVHMHMKKGINTLIMSLRGQDDPTPPSRINHERL 968
Db 1 NPDHARNSLNCGIROPKYGDVHMHMKKGINTLIMSLRGQDDPTPPSRINHERL 60

QY 969 EPLGDVAVPELTSVHLIYLPSPSEEGGLATYRTAIVQNHSLAMAKKLELDPMLVAHGP 1028
Db 61 EPLGDVAVPELTSVHLIYLPSPSEEGGLATYRTAIVQNHSLAMAKKLELDPMLVAHGP 120

QY 1029 DLRCSDLRHAMANCEALIGAVYLGSLSEAEKQLFGRLLFNDPDLREVWLNYPHLPQL 1088
Db 121 DLRCSDLRHAMANCEALIGAVYLGSLSEAEKQLFGRLLFNDPDLREVWLNYPHLPQL 180

QY 1089 QEPNTRQLIETSPVLQKLTPEFEAIGVIFTHVRLARAPTLRTVGFNHLTLGHNMREF 1148
Db 181 QEPNTRQLIETSPVLQKLTPEFEAIGVIFTHVRLARAPTLRTVGFNHLTLGHNMREF 240

QY 1149 LQDSIMQVATEYLFTHFPDHHGHLLTLSSLVNRTQAKVABELGMQYAITNDKTKR 1208
Db 241 LQDSIMQVATEYLFTHFPDHHGHLLTLSSLVNRTQAKVABELGMQYAITNDKTKR 300

QY 1209 PVGLRTKTLADLLESFIAALYTDKLEYVHTFMNVCFPPRLKEFILNQDNDPKSQLOQC 1268
Db 301 PVGLRTKTLADLLESFIAALYTDKLEYVHTFMNVCFPPRLKEFILNQDNDPKSQLOQC 360

QY 1269 CLTLRTGKPEDIPLYKTLQTVGSPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMD 1328
Db 361 CLTLRTGKPEDIPLYKTLQTVGSPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMD 420

QY 1329 LEKYNPQMAHQKRFGRKYRQELKEMREREHOREPDEDEIKK 1374
Db 421 LEKYNPQMAHQKRFGRKYRQELKEMREREHOREPDEDEIKK 466

RESULT 11
US-10-103-313-471
; Sequence 471, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ07C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 471
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-313-471

Query Match      26.1%; Score 1961; DB 4; Length 378;
Best Local Similarity 98.9%; Pred. No. 4.9e-112;
Matches 374; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 997 ATYRTAIVQNHSLAMAKKLELDPMLVAHGPDLCRSDLRHAMANCEALIGAVYLEGS 1056
Db 1 ATYRTAIVQNHSLAMAKKLELDPMLVAHGPDLCRSDLRHAMANCEALIGAVYLEGS 60

QY 1057 LEEAKQLFGRLLFNDPDLREVWLNYPHLPQLQEPNTRQLIETSPVLQKLTPEFEAIGV 1116
Db 61 LEEAKQLFGRLLFNDPDLREVWLNYPHLPQLQEPNTRQLIETSPVLQKLTPEFEAIGV 120

QY 1117 IFTHVRLARAPTLRTVGFNHLTLGHNMREFLQDSIMQVATEYLFTHFPDHHGHLLTL 1176
Db 1176 IFTHVRLARAPTLRTVGFNHLTLGHNMREFLQDSIMQVATEYLFTHFPDHHGHLLTL 180

QY 1177 LRSSLVNNRTQAKVABELGMQYAITNDKTKRPVGLRTKTLADLLESFIAALYTDKLEY 1236
Db 181 LRSSLVNNRTQAKVABELGMQYAITNDKTKRPVGLRTKTLADLLESFIAALYTDKLEY 240

QY 1237 VHTFMNVCFPPRLKEFILNQDNDPKSQLOQCCLTLRTGKPEDIPLYKTLQTVGSPSHAR 1296
Db 241 VHTFMNVCFPPRLKEFILNQDNDPKSQLOQCCLTLRTGKPEDIPLYKTLQTVGSPSHAR 300

QY 1297 YTVAVYFKGERIGCGKGPSIQQAEMGAAMDALKEKNFPMQAHQKRFGRKYRQELKEMR 1356
Db 301 YTVAVYFKGERIGCGKGPSIQQAEMGAAMDALKEKNFPMQAHQKRFGRKYRQELKEMR 360

QY 1357 WEREHOREPDEDEIKK 1374
Db 361 WEREHOREPDEDEIKK 378

RESULT 12
US-10-103-313-307
; Sequence 307, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ07C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 307
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-313-307

Query Match      17.6%; Score 1320; DB 4; Length 263;
Best Local Similarity 97.7%; Pred. No. 6.7e-73;
Matches 251; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1118 FTHVRLARAPTLRTVGFNHLTLGHNMREFLQDSIMQVATEYLFTHFPDHHGHLLTL 1177
Db 7 FTHVRLARAPTLRTVGFNHLTLGHNMREFLQDSIMQVATEYLFTHFPDHHGHLLTL 66

QY 1178 LRSSLVNNRTQAKVABELGMQYAITNDKTKRPVGLRTKTLADLLESFIAALYTDKLEY 1237
Db 67 LRSSLVNNRTQAKVABELGMQYAITNDKTKRPVGLRTKTLADLLESFIAALYTDKLEY 126

QY 1238 HTFMNVCFPPRLKEFILNQDNDPKSQLOQCCLTLRTGKPEDIPLYKTLQTVGSPSHART 1297
Db 127 HTFMNVCFPPRLKEFILNQDNDPKSQLOQCCLTLRTGKPEDIPLYKTLQTVGSPSHART 186

QY 1298 YTVAVYFKGERIGCGKGPSIQQAEMGAAMDALKEKNFPMQAHQKRFGRKYRQELKEMR 1357
Db 187 YTVAVYFKGERIGCGKGPSIQQAEMGAAMDALKEKNFPMQAHQKRFGRKYRQELKEMR 246

QY 1358 WEREHOREPDEDEIKK 1374
Db 247 WEREHOREPDEDEIKK 263

RESULT 13
US-09-900-425A-3
; Sequence 3, Application US/09900425A
; Patent No. US20020164601A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Hongjiang
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Human RNase III and Compositions and Uses Thereof
; FILE REFERENCE: ISPH-0522
; CURRENT APPLICATION NUMBER: US/09/900,425A
```


Query Match 11.9%; Score 890; DB 3; Length 412;
Best Local Similarity 43.1%; Pred. No. 3e-46;
Matches 181; Conservative 85; Mismatches 136; Indels 18; Gaps 7;
944 TLINIMSLGQDDPTPSRINHNRLERFLGDAVVEFLTSVHLVYLPFSLBEGGLATYRTAI 1003
2 SLFNIMKGTSGGEP-----ILHNERLYLGDVAVVELIVSHHLYFMLTHHFEGLATYRTAL 57
1004 VQNHMLAKKLELDPFMYAHGPDLCRESDLRHAMANCEALIGAVYLEGSLEAKQL 1063
58 VQNRNLATLAKNCRIDEMQLQYSHGADLINVAEFKHALANAFEAAMAIYLDGGLAPCDVI 117
1064 FGRLLF-NDPDLREVWNLPLHPLQEQPNTDRLQIETSPVLOKLTFFEEAIGVIFTHVR 1122
118 FSKAMYGHQVPLKEKWDHINEHLKREDPQGDRLDSFITPTLSTFHAEERLGIQFNIR 177
1123 LLARAFTLRTVGNHLLTLGHNMREFLGDIMOLVATEYLFIHFPDHHGHLTLRLSSLV 1182
178 LLAKAFTRRNIPNNDLTGHNQRLWGLDGLVQLIVSDFLYRRFPYHHEGMSLLRTSLV 237
1183 NNRTQAKVABEELCMQYAITNDKTPV---GLRTKTLADLLESFIAALYTDKLEVVHT 1239
238 SNQTAQVCCDLDLGFTEFVI-----KAPYKTPPELKKADLVFAFAGALVVDRGIEHCRA 292
1240 FMNVCFPRLKEFILNODWNPDSQLOQCCLTLR-TEGKEPDIPLYKTLQTVGPSHARTY 1298
293 FIRIVECPRLKHFIESEKNDAKSHLQOWCLAMRDPSSSEPDMPYRVLGIEGPTNNRIF 352
1299 TVAVYKGERIGCGKPSIQOAEWGA---AMDALKYNNPQM-AHQKRFGRKYRQELKE 1354
353 KIAVYKGRKLSAASNSVHKAELRVAELALANLESMSFSKMAKNNSNRRRLEQDTS 412

RESULT 14
US-10-079-185-3
; Sequence 3, Application US/10079185
; Publication No. US20030044941A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof
; FILE REFERENCE: IS185030
; CURRENT APPLICATION NUMBER: US/10/079,185
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 09/479,783
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 08/870,608
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 08/659,440
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 09/900,425
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-079-185-3

Query Match 11.9%; Score 890; DB 4; Length 412;
Best Local Similarity 43.1%; Pred. No. 3e-46;
Matches 181; Conservative 85; Mismatches 136; Indels 18; Gaps 7;
944 TLINIMSLGQDDPTPSRINHNRLERFLGDAVVEFLTSVHLVYLPFSLBEGGLATYRTAI 1003
2 SLFNIMKGTSGGEP-----ILHNERLYLGDVAVVELIVSHHLYFMLTHHFEGLATYRTAL 57
1004 VQNHMLAKKLELDPFMYAHGPDLCRESDLRHAMANCEALIGAVYLEGSLEAKQL 1063
58 VQNRNLATLAKNCRIDEMQLQYSHGADLINVAEFKHALANAFEAAMAIYLDGGLAPCDVI 117
1064 FGRLLF-NDPDLREVWNLPLHPLQEQPNTDRLQIETSPVLOKLTFFEEAIGVIFTHVR 1122
118 FSKAMYGHQVPLKEKWDHINEHLKREDPQGDRLDSFITPTLSTFHAEERLGIQFNIR 177
1123 LLARAFTLRTVGNHLLTLGHNMREFLGDIMOLVATEYLFIHFPDHHGHLTLRLSSLV 1182
178 LLAKAFTRRNIPNNDLTGHNQRLWGLDGLVQLIVSDFLYRRFPYHHEGMSLLRTSLV 237
1183 NNRTQAKVABEELCMQYAITNDKTPV---GLRTKTLADLLESFIAALYTDKLEVVHT 1239
238 SNQTAQVCCDLDLGFTEFVI-----KAPYKTPPELKKADLVFAFAGALVVDRGIEHCRA 292
1240 FMNVCFPRLKEFILNODWNPDSQLOQCCLTLR-TEGKEPDIPLYKTLQTVGPSHARTY 1298
293 FIRIVECPRLKHFIESEKNDAKSHLQOWCLAMRDPSSSEPDMPYRVLGIEGPTNNRIF 352
1299 TVAVYKGERIGCGKPSIQOAEWGA---AMDALKYNNPQM-AHQKRFGRKYRQELKE 1354
353 KIAVYKGRKLSAASNSVHKAELRVAELALANLESMSFSKMAKNNSNRRRLEQDTS 412

RESULT 15
US-10-774-974-3
; Sequence 3, Application US/10774974
; Publication No. US20040126867A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Hongjiang
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof
; FILE REFERENCE: IS185029/ISPH-0522
; CURRENT APPLICATION NUMBER: US/10/774,974
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: US/09/900,425B
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-774-974-3

Query Match 11.9%; Score 890; DB 4; Length 412;
Best Local Similarity 43.1%; Pred. No. 3e-46;
Matches 181; Conservative 85; Mismatches 136; Indels 18; Gaps 7;
944 TLINIMSLGQDDPTPSRINHNRLERFLGDAVVEFLTSVHLVYLPFSLBEGGLATYRTAI 1003
2 SLFNIMKGTSGGEP-----ILHNERLYLGDVAVVELIVSHHLYFMLTHHFEGLATYRTAL 57
1004 VQNHMLAKKLELDPFMYAHGPDLCRESDLRHAMANCEALIGAVYLEGSLEAKQL 1063
58 VQNRNLATLAKNCRIDEMQLQYSHGADLINVAEFKHALANAFEAAMAIYLDGGLAPCDVI 117
1064 FGRLLF-NDPDLREVWNLPLHPLQEQPNTDRLQIETSPVLOKLTFFEEAIGVIFTHVR 1122
118 FSKAMYGHQVPLKEKWDHINEHLKREDPQGDRLDSFITPTLSTFHAEERLGIQFNIR 177
1123 LLARAFTLRTVGNHLLTLGHNMREFLGDIMOLVATEYLFIHFPDHHGHLTLRLSSLV 1182

Db	178	LLAKAFTRRNIPNNDLTKGHNQRLWLGDSVLQLIVSDFLYRRFPYHHEGHMSLLRTSLV	237
Qy	1183	NNKTOAKVAEELGMOBYAITNDKTRPV---GLRTKTLADLLESPIAALYTDKLEYVHT	1239
Db	238	SNQTOAVVCCDLGTFEVI-----KAPYKTPPELKLKADLVEAFICALYVDRGIEHCRA	292
Qy	1240	FMNVCFPRLEKEFILNQDNDPKSQLQCCCLTLR-TEGKEPDIPLYKTLQTVGSPSHARTY	1298
Db	293	FIRIVFCPRLEKHFIESEKWNDAKSHLQQWCLAWDFSSSEPDMPFYRVLGIEGFTNNRIF	352
Qy	1299	TVAVYFKGERIGCGKGPSIQQAEMGA---AMDALKEYNFPQM-AHQKRFIGRKYQELKE	1354
Db	353	KIAVYKGRKLASAAESNVHKAEIRVAELALANLESMSFSKMKAKNNSNNRRELEQDTS	412

Search completed: December 24, 2005, 01:02:56
Job time : 198 secs

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OM protein - protein search, using sw model

Run on: December 24, 2005, 00:32:40 ; Search time 202 Seconds
(without alignments)
2988.646 Million cell updates/sec

Title: US-10-774-974-2
Perfect score: 7500
Sequence: 1 MQQNTCHMSFHPGRCPR.....MRWERHQREPDTEDIKK 1374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7500	100.0	1374	8 ADQ96675	Adq96675 Human rib
2	7500	100.0	1374	8 ADR68727	Adr68727 Human rib
3	7500	100.0	1374	9 AEB47411	Aeb47411 Human rib
4	7486	99.8	1374	8 ADQ17464	Adq17464 Human sof
5	7486	99.8	1374	9 ADY17386	Ady17386 PRO polyp
6	7483.5	99.8	1373	7 ABU63361	Abu63361 Human dou
7	6426	85.7	1200	9 AEA20195	Aea20195 Novel hum
8	6062	80.8	1374	6 ABU08060	Abu08060 Human RNA
9	4071	54.3	769	4 AAB32635	Aab32635 Human pro
10	2963	39.5	1327	4 ABB58539	Abb58539 Drosophil
11	2847	38.0	541	6 ABM04841	Abm04841 Human put
12	2519	33.6	486	9 AEA21037	Aea21037 Novel hum
13	2463	32.8	466	8 ADQ96710	Adq96710 Human rib
14	1961	26.1	378	4 AAU20587	Aau20587 Human sec
15	1961	26.1	378	4 AAU21744	Aau21744 Novel hum
16	1961	26.1	378	7 ADC46385	Adc46385 Human neo
17	1956	26.1	378	4 AAU20385	Aau20385 Human sec
18	1320	17.6	263	4 AAU21580	Aau21580 Novel hum
19	1320	17.6	263	7 ADC46221	Adc46221 Human neo
20	1295.5	17.3	301	4 AAB63281	Aab63281 Human bre
21	1289	17.2	267	4 AAB63379	Aab63379 Human bre
22	1122	15.0	277	4 AAB63383	Aab63383 Human bre
23	890	11.9	412	8 ADQ96676	Adq96676 Caenorhab
24	890	11.9	412	8 ADR68728	Adr68728 C. elegans

25	890	11.9	412	9 AEB47412	Aeb47412 Nematode
26	702	9.4	148	5 ADK34912	Adk34912 Novel hum
27	496	6.6	115	2 AAY12224	Aay12224 Human 5'
28	496	6.6	115	3 AAG00554	Aag00554 Human sec
29	472	6.3	97	5 ABB10067	Abb10067 Human non
30	340	4.5	1151	4 ABB61598	Abb61598 Drosophil
31	312.5	4.2	241	7 ADC95807	Adc95807 E. faeciu
32	311	4.1	560	4 ABG21040	Abg21040 Novel hum
33	309	4.1	286	9 AEB48256	Aeb48256 Bacillus
34	307.5	4.1	229	5 ABB48891	Abb48891 Listeria
35	303.5	4.0	406	4 ABG27250	Abg27250 Novel hum
36	301.5	4.0	1663	8 ABM81721	Abm81721 Tumour-as
37	298.5	4.0	228	5 ABP30268	Abp30268 Streptoco
38	298.5	4.0	228	8 ADV88449	Adv88449 Streptoco
39	298.5	4.0	228	8 ADV81861	Adv81861 Streptoco
40	298.5	4.0	228	8 ADV79702	Adv79702 Streptoco
41	298.5	4.0	242	5 ABP25995	Abp25995 Streptoco
42	297.5	4.0	800	8 ABO58564	Abos58564 Human gen
43	285.5	3.8	225	9 AEB48251	Aeb48251 Vibrio ch
44	285.5	3.8	1527	8 ADU47047	Adu47047 Corn Dice
45	285.5	3.8	1636	8 ADU47051	Adu47051 Corn Dice

ALIGNMENTS

RESULT 1

ADQ96675
ID ADQ96675 standard; protein; 1374 AA.

XX AC ADQ96675;
XX XX
DT 23-SBP-2004 (first entry)
XX XX
DE Human ribonuclease III (RNase III) enzyme.

KW Human; ribonuclease III; RNase III; research purpose; biological purpose;
KW clinical purpose; cellular interaction; enzyme.
XX Homo sapiens.

OS
FH Key Location/Qualifiers
FT Region 1..220
FT Misc-difference 18 /note= "Proline rich region"
FT Region 221..470 /note= "Encoded by CGT"
FT Domain 949..1374 /note= "Serine-arginine rich region"
FT Misc-difference 1211 /note= "RNase III domain"
FT Region 1262..1269 /note= "Encoded by GCG"
FT Region 1282..1290 /note= "Alpha helix"
FT Region 1297..1303 /note= "Beta sheet"
FT Region 1308..1315 /note= "Beta sheet"
FT Region 1316..1336 /note= "Beta sheet"
FT Misc-difference 1345 /note= "Alpha helix"
FT US2004126867-A1. /note= "Encoded by GAA"

XX
PN 01-JUL-2004.
XX
PD 09-FEB-2004; 2004US-00774974.
XX
PF 06-JUL-2001; 2001US-00900425.
XX

PA (CROO/) CROOKE S T.
PA (WUHH/) WU H.
XX Crooke ST, Wu H;
PI
DR WPI; 2004-516913/49.
DR N-PSDB; ADQ96674.
XX
XX New isolated nucleic acid molecule encoding human RNase III, useful for
PT research, biological, or clinical purposes, e.g. defining the roles of
PT RNase III and the interaction of human RNase III and cellular RNA.
PS
PS Claim 3; SEQ ID NO 2; 31pp; English.
XX
XX The invention relates to human ribonuclease III (RNase III) and its
CC corresponding nucleic acid sequence. The polynucleotide sequence of the
CC invention is useful for research, biological and clinical purposes. It is
CC useful in defining the roles of RNase III and the interaction of human
CC RNase III and cellular RNA. The present sequence is the human RNase III
CC enzyme.
XX
SQ Sequence 1374 AA;
Query Match 100.0%; Score 7500; DB 8; Length 1374;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMQGNTRCHMSFHPGRCGRGCHGARGSPAFRPNLRLLHPQQPPVQYQVEPPSAPS 60
Db 1 MMQGNTRCHMSFHPGRCGRGCHGARGSPAFRPNLRLLHPQQPPVQYQVEPPSAPS 60
QY 61 TTFSNSPAPNLFDPDFVFPFPPMPSAQGLPPCPPIRPPFPHQWRHPPFVPPCFPPM 120
Db 61 TTFSNSPAPNLFDPDFVFPFPPMPSAQGLPPCPPIRPPFPHQWRHPPFVPPCFPPM 120
QY 121 PPMPCPNPPVPGAPPGQGTFFPMPPPSMPHPPPPVMPQOVNTQYPPGYSHNFPFPP 180
Db 121 PPMPCPNPPVPGAPPGQGTFFPMPPPSMPHPPPPVMPQOVNTQYPPGYSHNFPFPP 180
QY 181 SFNSFQNNPSSFLPSANNSSPHRLPPYPLPKAPSERRSERLKHDDHRDHSRGR 240
Db 181 SFNSFQNNPSSFLPSANNSSPHRLPPYPLPKAPSERRSERLKHDDHRDHSRGR 240
QY 241 GERHSLDRERGRSPDRRQDSRYSDYDGRGTPSHRSYERSRERERHHRNRRS 300
Db 241 GERHSLDRERGRSPDRRQDSRYSDYDGRGTPSHRSYERSRERERHHRNRRS 300
QY 301 PSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIKNVDSWAPPLEIVNHRSPSREK 360
Db 301 PSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIKNVDSWAPPLEIVNHRSPSREK 360
QY 361 KRARWEEKDRWSDNOSGKDKNYTSIKEKEPEETMPDKNEEEELLKPVWIRCTHSEN 420
Db 361 KRARWEEKDRWSDNOSGKDKNYTSIKEKEPEETMPDKNEEEELLKPVWIRCTHSEN 420
QY 421 YYSDDPMDQVGDSTVGTSLRLDYKFEELSGRQEKAKAAPPPWPPPKTKLDELESS 480
Db 421 YYSDDPMDQVGDSTVGTSLRLDYKFEELSGRQEKAKAAPPPWPPPKTKLDELESS 480
QY 481 SESECEDESDTSCSSSDSEVDVIAIRKKAHPDRHDELWYNDPGQMDGPKLCKSA 540
Db 481 SESECEDESDTSCSSSDSEVDVIAIRKKAHPDRHDELWYNDPGQMDGPKLCKSA 540
QY 541 KARRTGIRHSIYPGEEAIKFCRPMNNAAGLFHYRITVSPPTNFLTDRPTVIEYDDHEYI 600
Db 541 KARRTGIRHSIYPGEEAIKFCRPMNNAAGLFHYRITVSPPTNFLTDRPTVIEYDDHEYI 600
QY 601 FEGFSMFAHAPLNTIPLCKVIRFNIDYTHFIEEMMPENFCVKGLELFSFLFRDILELY 660
Db 601 FEGFSMFAHAPLNTIPLCKVIRFNIDYTHFIEEMMPENFCVKGLELFSFLFRDILELY 660
QY 661 DWNLKGPLFSDSPCCPRFHPMRFVFLPDGGKVELSMHQIILLYLLRCSKALVPDEEIA 720
Db 661 DWNLKGPLFSDSPCCPRFHPMRFVFLPDGGKVELSMHQIILLYLLRCSKALVPDEEIA 720

Db 661 DWNLKGPLFSDSPCCPRFHPMRFVFLPDGGKVELSMHQIILLYLLRCSKALVPDEEIA 720
QY 721 NMLQWEELEWQYABECKGMIVTNGTKPSSVRIDQLDREQFNPDVITPIIVHFGIRPA 780
Db 721 NMLQWEELEWQYABECKGMIVTNGTKPSSVRIDQLDREQFNPDVITPIIVHFGIRPA 780
QY 781 QLSYAGDPOYQKLWKSYYVKLRHLLANS PKVQTDKQKLAQREBEALQKTRQKNTMRREVTV 840
Db 781 QLSYAGDPOYQKLWKSYYVKLRHLLANS PKVQTDKQKLAQREBEALQKTRQKNTMRREVTV 840
QY 841 ELSQGFWKGTGRSDVCQHMMMLPVLTHIRVHOCIMHLDKLIQYTFQDRCCLQLAMWHP 900
Db 841 ELSQGFWKGTGRSDVCQHMMMLPVLTHIRVHOCIMHLDKLIQYTFQDRCCLQLAMWHP 900
QY 901 SHLHNGMNDPHARNLSNCGIRQPKYGDVKVHHMHRKKGINTLINIMSRIGQDDPTPS 960
Db 901 SHLHNGMNDPHARNLSNCGIRQPKYGDVKVHHMHRKKGINTLINIMSRIGQDDPTPS 960
QY 961 RINHNERLEFLGDVAVVEFLTSVHLVYLPFSLBEGGLATVYRTAIVQNHMLAKKLELDP 1020
Db 961 RINHNERLEFLGDVAVVEFLTSVHLVYLPFSLBEGGLATVYRTAIVQNHMLAKKLELDP 1020
QY 1021 FMLYAHGPDLCRESDLRHMANCFEALIGAVYLEGSLEBAKOLFGEILLFNDPDLREVWLN 1080
Db 1021 FMLYAHGPDLCRESDLRHMANCFEALIGAVYLEGSLEBAKOLFGEILLFNDPDLREVWLN 1080
QY 1081 YPLHPLQLOEPNTDQOLIETSPVLOKLTFFEBEAGVIFTHVRLARAFTRVGFNHLTL 1140
Db 1081 YPLHPLQLOEPNTDQOLIETSPVLOKLTFFEBEAGVIFTHVRLARAFTRVGFNHLTL 1140
QY 1141 GHNQRMFELGDSIMQIVATEYLFIHPFDHHEGLTLRLSSLVNNRTQAKVABELGMOEYA 1200
Db 1141 GHNQRMFELGDSIMQIVATEYLFIHPFDHHEGLTLRLSSLVNNRTQAKVABELGMOEYA 1200
QY 1201 ITNDTKRPVGLRKTTLADLLSSFTAAALYTDKOLEVYVHTFMVVCFFPRLKEFLINQDWD 1260
Db 1201 ITNDTKRPVGLRKTTLADLLSSFTAAALYTDKOLEVYVHTFMVVCFFPRLKEFLINQDWD 1260
QY 1261 PKSOLOQCCLTARTEGKPDIPLYKTLQVGPSHARTYVAVYFKGERICGCGPSIQQA 1320
Db 1261 PKSOLOQCCLTARTEGKPDIPLYKTLQVGPSHARTYVAVYFKGERICGCGPSIQQA 1320
QY 1321 EMGAAMDALKENYFPOMAHQKFGIKRYQELKEMWEREHQREPEDETDIKK 1374
Db 1321 EMGAAMDALKENYFPOMAHQKFGIKRYQELKEMWEREHQREPEDETDIKK 1374
RESULT 2
ADR68727
ID ADR68727 standard; protein; 1374 AA.
XX ADR68727;
DT
DT 02-DEC-2004 (first entry)
XX Human Ribonuclease III, RNase III.
XX Human; enzyme; Ribonuclease III; RNase III; RNA interference;
KW gene silencing; double stranded RNA; pre-rRNA processing; RNA processing;
KW RNA expression; RNA splicing; RNA translocation.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1. .220
FT /label = Proline rich domain 1320
FT /note= "Claimed in claim 8"
FT Domain
FT 221. .470
FT /label = Serine Arginine rich domain
FT /note= "Claimed in claim 8"
FT 949. .1374
FT /label = RNase III domain
FT /note= "Claimed in claim 8"

Db	1321	EMGAAMDALEKYNFPQMAHQKRFGRIGRQELKEMWREHQBREPDETDIKK	1374
RESULT 3			
ID	AEB47411		
AC	AEB47411	standard; protein; 1374 AA.	
XX			
DT	22-SEP-2005	(first entry)	
DE	Human ribonuclease III (RNase III) protein, SEQ ID NO: 2.		
XX			
KW	Ribonuclease; gene silencing; enzyme.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Region	1..220	/note= "RNase III proline-rich region"
FT	Misc-difference	18	/note= "Encoded by CGT"
FT	Region	221..470	/note= "RNase III serine-arginine rich region"
FT	Domain	949..1374	
FT	Misc-difference	1211	/note = RNase III domain
FT	Region	1262..1269	/note= "Encoded by GCG"
FT	Region	1282..1290	/note= "Alpha helix"
FT	Region	1297..1303	/note= "Beta sheet"
FT	Region	1308..1315	/note= "Beta sheet"
FT	Region	1318..1336	/note= "Alpha helix"
FT	Misc-difference	1345	/note= "Encoded by GAA"
XX	US2005159384-A1.		
XX	21-JUL-2005.		
XX	02-DEC-2004; 2004US-00001993.		
XX	06-JUL-2001; 2001US-00900425.		
PR	20-FEB-2002; 2002US-00079185.		
XX	(ISIS-) ISIS PHARM INC.		
XX	Crooke ST;		
XX	WPI; 2005-512270/52.		
DR	N-PSDB; AEB47410.		
DR	GENBANK; AAF80558.		
XX	Use of RNase III for eliciting modification of a selected RNA target,		
PT	promoting gene silencing of a gene, inhibiting the expression of a gene,		
PT	promoting inhibition of expression of a gene, or eliciting modification		
PT	of an RNA target.		
XX	Claim 19; SEQ ID NO 2; 32pp; English.		
XX	The present invention relates to ribonuclease III (RNase III) nucleic		
CC	acids and their encoding proteins. RNase III is an endoribonuclease that		
CC	cleaves double stranded RNA. The invention is useful for eliciting		
CC	modification of a selected RNA target in a cell, promoting gene silencing		
CC	of a gene, inhibiting the expression of a gene, promoting inhibition of		
CC	expression of a gene and eliciting modification of a RNA target in a		
CC	cell. The present sequence is human ribonuclease III (RNase III) protein.		

SQ	Sequence	1374 AA;	
	Query Match	100.0%; Score 7500; DB 9; Length 1374;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 1374; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MMQGNCTCHRMSPHPCGRCGRGGHGAAPSAPSPQNRLRLHPQPPVQVQYQVEPPSAPS	60
Db	1	MMQGNCTCHRMSPHPCGRCGRGGHGAAPSAPSPQNRLRLHPQPPVQVQYQVEPPSAPS	60
QY	61	TTFSNSPAPNLFPPRDPFVFPFPPMPPSAQGLPCPTPFPFNHOMRPPVPPPCFPPM	120
Db	61	TTFSNSPAPNLFPPRDPFVFPFPPMPPSAQGLPCPTPFPFNHOMRPPVPPPCFPPM	120
QY	121	PPMPCNNPPVPAGPPGQGTFFFMPPMPPMPPPPVMPQQVNVYQYPPGYSHNFPPP	180
Db	121	PPMPCNNPPVPAGPPGQGTFFFMPPMPPMPPPPVMPQQVNVYQYPPGYSHNFPPP	180
QY	181	SFNSFQNNPSSFLPSANNSSSPHFRHLPYPLPKAPSERRSERLKHYYDDHRRDHSGR	240
Db	181	SFNSFQNNPSSFLPSANNSSSPHFRHLPYPLPKAPSERRSERLKHYYDDHRRDHSGR	240
QY	241	GERHSLDRRERGRSPDRRQDSRYRSYDRGRTSRHRSYRSRERERHRRDRNR	300
Db	241	GERHSLDRRERGRSPDRRQDSRYRSYDRGRTSRHRSYRSRERERHRRDRNR	300
QY	301	PSLERSYKKEYKRSGRSYGLSVVPRPAGCTPELPGEIIKNTDSWAPPLIIVNHRSPREK	360
Db	301	PSLERSYKKEYKRSGRSYGLSVVPRPAGCTPELPGEIIKNTDSWAPPLIIVNHRSPREK	360
QY	361	KEARWEEEEKDRWSDNQSSGDKNYTISIKEKPEETMPDKNEEEELLKPVWIRCTHSEN	420
Db	361	KEARWEEEEKDRWSDNQSSGDKNYTISIKEKPEETMPDKNEEEELLKPVWIRCTHSEN	420
QY	421	YYSSDPMDQVGDSTVVGTSRLRLDYDKFBEELGSRQEKAKAAPPEPKTKLDELESS	480
Db	421	YYSSDPMDQVGDSTVVGTSRLRLDYDKFBEELGSRQEKAKAAPPEPKTKLDELESS	480
QY	481	SESECESDESDTSCSSSSDSEVDFVIAEIKRKAHPDRLHDELWYNDPGQWMDGPKC	540
Db	481	SESECESDESDTSCSSSSDSEVDFVIAEIKRKAHPDRLHDELWYNDPGQWMDGPKC	540
QY	541	KARRTGIRHSIYPGEAAIKPCRPMTNNAAGRLFHYRITVSPPTNFLTDRPTVIEYDDHE	600
Db	541	KARRTGIRHSIYPGEAAIKPCRPMTNNAAGRLFHYRITVSPPTNFLTDRPTVIEYDDHE	600
QY	601	FEFGSMFAHAPLTNIPLCVKIRPNIDYTHFTIEMMPENFCVKGLFSLFLFRDILELY	660
Db	601	FEFGSMFAHAPLTNIPLCVKIRPNIDYTHFTIEMMPENFCVKGLFSLFLFRDILELY	660
QY	661	DMNLKGLPFEDSPCCPRFHEMFRFVRFLPDGGSKEVLSMHQIILLYLLRCSKALVP	720
Db	661	DMNLKGLPFEDSPCCPRFHEMFRFVRFLPDGGSKEVLSMHQIILLYLLRCSKALVP	720
QY	721	NMLQWEELEWQKYAECKGMIVTNPCTKPSVVRIDQLDREQFNPDVITPPIIVHFGIR	780
Db	721	NMLQWEELEWQKYAECKGMIVTNPCTKPSVVRIDQLDREQFNPDVITPPIIVHFGIR	780
QY	781	QLSYAGDPQYQKLWKSIVKLRHLLANSVKVQTDKQKLAQREALOKIRKQNTMRRE	840
Db	781	QLSYAGDPQYQKLWKSIVKLRHLLANSVKVQTDKQKLAQREALOKIRKQNTMRRE	840
QY	841	ELSSQGFQWKTGIRSDYCOHAMMLPVLTHIRVHQCILMHLDKLIGYTFQDRCLLQ	900
Db	841	ELSSQGFQWKTGIRSDYCOHAMMLPVLTHIRVHQCILMHLDKLIGYTFQDRCLLQ	900
QY	901	SHHLNFGMPDHDARNLSLNCIGIRQPKYGRKRVHMHMRKKGINTLINMSRLQGDD	960
Db	901	SHHLNFGMPDHDARNLSLNCIGIRQPKYGRKRVHMHMRKKGINTLINMSRLQGDD	960
QY	961	RINHNERLEFLGDVAVFEFLTSVHLIYFLPSLEGGIATYRTAIVQNOHLAMLA	1020
Db	961	RINHNERLEFLGDVAVFEFLTSVHLIYFLPSLEGGIATYRTAIVQNOHLAMLA	1020

QY 1021 FMLYAHGPDLCRESDLRHANCFEALIGAVYLEGSLLEBAKOLFGRLLFNDPDLREVWLN 1080
DB |||||
QY 1021 FMLYAHGPDLCRESDLRHANCFEALIGAVYLEGSLLEBAKOLFGRLLFNDPDLREVWLN 1080
DB |||||
QY 1081 YPLHPLQLQBPNTDROLIETSPVLQKLTPEEAIGVIFTHVRLARAFRTLTGVFNHLLT 1140
DB |||||
QY 1081 YPLHPLQLQBPNTDROLIETSPVLQKLTPEEAIGVIFTHVRLARAFRTLTGVFNHLLT 1140
DB |||||
QY 1141 GHNQMEFLGDSIMQLVATEYLFTHPPDHHEGLTLRLSSLVNVRTQAKVAEELGMOEYA 1200
DB |||||
QY 1201 ITNDKTRPVGLRTKTLADLLESFIAALYTDKOLEYVHTFMNVCFPPRLKEFLINQDWD 1260
DB |||||
QY 1261 ITNDKTRPVGLRTKTLADLLESFIAALYTDKOLEYVHTFMNVCFPPRLKEFLINQDWD 1260
DB |||||
QY 1261 PKSQLQCCCLTLTEGKEPDIPLYKTLQTVGPHSHARTYTVAVYFKGERICGKGPSIQQA 1320
DB |||||
QY 1321 EMGAAMDALEKYNFPQMAHQKFRIGRYQELKEMRWEREHQREPEDETIKK 1374
DB |||||
QY 1321 EMGAAMDALEKYNFPQMAHQKFRIGRYQELKEMRWEREHQREPEDETIKK 1374
DB |||||

RESULT 4

ADQ17464
ID ADQ17464 standard; protein; 1374 AA.
AC ADQ17464;
XX
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 281.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
OS Homo sapiens.
XX
XX WO2004048938-A2.
XX
XX 10-JUN-2004.
XX
XX 26-NOV-2003; 2003WO-US038193.
XX
XX 26-NOV-2002; 2002US-0429739P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Aziz N, Ginsburg WM, Zlotnik A;
XX
XX WPI; 2004-441208/41.
XX
XX

PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.

PS Example 2; SEQ ID NO 281; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the

CC specification per se but was submitted in CD format by the inventor.

XX SQ Sequence 1374 AA;
Query Match 99.8%; Score 7486; DB 8; Length 1374;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1372; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MMQGNCTCHMSFHPGRCGRGCHGARSAPSRPQNLALLHPQPPVQYQVEPPSAPS 60
DB |||||
QY 1 MMQGNCTCHMSFHPGRCGRGCHGARSAPSRPQNLALLHPQPPVQYQVEPPSAPS 60
DB |||||
QY 61 TTFSNSPAPNLFPRDFVFPFPPMPPSAGPLPCCPIRPFPHNQMRHFPFVPCPPPM 120
DB |||||
QY 61 TTFSNSPAPNLFPRDFVFPFPPMPPSAGPLPCCPIRPFPHNQMRHFPFVPCPPPM 120
DB |||||
QY 121 PPMPCPNPPVPVPCAPGGQTFPFMMPPPSMHPPPPVPVMPQVQVQYQPGYSHHNPFP 180
DB |||||
QY 121 PPMPCPNPPVPVPCAPGGQTFPFMMPPPSMHPPPPVPVMPQVQVQYQPGYSHHNPFP 180
DB |||||
QY 181 SFNSPQNPPSSFLPSANSSSPHFRHLPPYPLPKAPSERRSPERLKHYYDHRHDHSHGR 240
DB |||||
QY 181 SFNSPQNPPSSFLPSANSSSPHFRHLPPYPLPKAPSERRSPERLKHYYDHRHDHSHGR 240
DB |||||
QY 241 GERHSLDRRCGRSPDRRRQDSRYSDYDRGCTPSRHSYERSRERERHRHRNRSS 300
DB |||||
QY 241 GERHSLDRRCGRSPDRRRQDSRYSDYDRGCTPSRHSYERSRERERHRHRNRSS 300
DB |||||
QY 301 PSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIINKTDSWAPPLEIVNHRSPREK 360
DB |||||
QY 301 PSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIINKTDSWAPPLEIVNHRSPREK 360
DB |||||
QY 361 KXARWEEKDRWSDNQSSGDKNYTTSIXEKEPEETMPDKNEEEBELLKPVWIRCTHSEN 420
DB |||||
QY 361 KXARWEEKDRWSDNQSSGDKNYTTSIXEKEPEETMPDKNEEEBELLKPVWIRCTHSEN 420
DB |||||
QY 421 YSSDDPMDQVGDSTVVGTSRLRLDYKFFEEELGSRQEKAAAPPPPEPKTKLDEDESS 480
DB |||||
QY 421 YSSDDPMDQVGDSTVVGTSRLRLDYKFFEEELGSRQEKAAAPPPPEPKTKLDEDESS 480
DB |||||
QY 481 SESECESDESDTSCSSSDSEVPDVAIEIKRKAHPDLRHLDELWYNDPQWMDGFLCKCSA 540
DB |||||
QY 481 SESECESDESDTSCSSSDSEVPDVAIEIKRKAHPDLRHLDELWYNDPQWMDGFLCKCSA 540
DB |||||
QY 541 KARTGIRHSIYPGEEAIKPCRPMTNNAGRLPHYRTVSPPTNFLTDRPTVIEYDDHEYI 600
DB |||||
QY 541 KARTGIRHSIYPGEEAIKPCRPMTNNAGRLPHYRTVSPPTNFLTDRPTVIEYDDHEYI 600
DB |||||
QY 601 FEGFSMFAHAPLTNIPLCVIRFNIDYTHFTBEEMPFNCVKGLFSLFLFRDILELY 660
DB |||||
QY 601 FEGFSMFAHAPLTNIPLCVIRFNIDYTHFTBEEMPFNCVKGLFSLFLFRDILELY 660
DB |||||
QY 661 DWNLKGFLFEDSPCCPRFHFMPRVFRLPDGSKVLSMHQIILLYLLRCSKALVPBEEIA 720
DB |||||
QY 661 DWNLKGFLFEDSPCCPRFHFMPRVFRLPDGSKVLSMHQIILLYLLRCSKALVPBEEIA 720
DB |||||
QY 721 NMLQWEELEWQKYAECKGMIVTNPCTKPSVRAIDQLDREQFNPDVITPPIIVHFGIRPA 780
DB |||||
QY 721 NMLQWEELEWQKYAECKGMIVTNPCTKPSVRAIDQLDREQFNPDVITPPIIVHFGIRPA 780
DB |||||
QY 781 QLSYAGDPOYQKLWKSYYVKLRHLLANSKPVQTDKQKLAQREBALQKIROKNTMRREVT 840
DB |||||
QY 781 QLSYAGDPOYQKLWKSYYVKLRHLLANSKPVQTDKQKLAQREBALQKIROKNTMRREVT 840
DB |||||
QY 841 ELSQQCFWKTGTRSDVCOHAMMLPVLTHIRYHQCILMHLDKLIGYTFQDRCLLQAMTHP 900
DB |||||
QY 841 ELSQQCFWKTGTRSDVCOHAMMLPVLTHIRYHQCILMHLDKLIGYTFQDRCLLQAMTHP 900
DB |||||
QY 901 SHHLNFGMNPDHARNSLSNCGIRQPKYGRKVVHMMMRKKGINTLINIMSLRQDDPTPS 960
DB |||||
QY 901 SHHLNFGMNPDHARNSLSNCGIRQPKYGRKVVHMMMRKKGINTLINIMSLRQDDPTPS 960
DB |||||
QY 961 RINHNERLBFGLDVAVVEFTVSHLYYLPFSLBEGGLATYRTAIVQNHILAMLAKEULDP 1020
DB |||||

||||| 661 RINHNRLFLGDAVVEFLTSVHLVYLFPSLEBGGATVYRTAIVQNOHLAMAKKLELDP 1020
1021 FMYAHGPDLCRESDLRHAMANCEALIGAVYLEGSLEBAKQLFGRLLFNDPDLREVWLN 1080
1021 FMYAHGPDLCRESDLRHAMANCEALIGAVYLEGSLEBAKQLFGRLLFNDPDLREVWLN 1080
1081 YPLHPLQLOEPNDTDLIETSPVLQKLTFFEBEAGVIFTHVRLARAFILRTVGFNHLTL 1140
1081 YPLHPLQLOEPNDTDLIETSPVLQKLTFFEBEAGVIFTHVRLARAFILRTVGFNHLTL 1140
1141 GHNORMEFLGDSIMQLVATEYLFIFHPDHHGHLTLRSSLVNNRTQAKVABELGMOEYA 1200
1141 GHNORMEFLGDSIMQLVATEYLFIFHPDHHGHLTLRSSLVNNRTQAKVABELGMOEYA 1200
1201 ITNDTKRPVGLRTKTLADLLESFIAALYTDKOLEVHTFMNVCFPPRLKEFILNQDWND 1260
1201 ITNDTKRPVGLRTKTLADLLESFIAALYTDKOLEVHTFMNVCFPPRLKEFILNQDWND 1260
1261 PKSLOQCCLTLTTEGKEPDIPLYKTQTVGPHSHARTYTVAVYFKGERIGCGKGPSIQOA 1320
1261 PKSLOQCCLTLTTEGKEPDIPLYKTQTVGPHSHARTYTVAVYFKGERIGCGKGPSIQOA 1320
1321 EMGAAMDALKYNFPQMAHQKRIEYKRYQELKEMWEREHQEREDEDEDIKK 1374
1321 EMGAAMDALKYNFPQMAHQKRIEYKRYQELKEMWEREHQEREDEDEDIKK 1374

RESULT 5
ADY17386
ID ADY17386 standard; protein; 1374 AA.
XX AC ADY17386;
XX DT 05-MAY-2005 (first entry)
XX DE PRO polypeptide SEQ ID NO 3192.
XX XX
XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Asthmatic;
KW Antiallergic; de; gene; diagnosis.
XX OS Homo sapiens.
XX XX
XX WO2005016962-A2.
XX PN 11-AUG-2004; 2004WO-US026249.
XX XX
XX PD 24-FEB-2005.
XX XX
XX 11-AUG-2004; 2004WO-US026249.
XX XX
XX 11-AUG-2003; 2003US-0493546P.
XX XX
XX (GETH) GENENTECH INC.
XX PA Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX PI WPI; 2005-182330/19.
XX XX
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX XX
XX Claim 8; SEQ ID NO 3192; 158pp; English.
XX XX
XX The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
CC polypeptide.
XX XX

SQ Sequence 1374 AA;
Query Match 99.8%; Score 7486; DB 9; Length 1374;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1372; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MMQGNCTCHRMSPHGRGCGPRGGHGAAPSAPFPQNLRLHLPQPPVQVQYEPSPAPS 60
DB 1 MMQGNCTCHRMSPHGRGCGPRGGHGAAPSAPFPQNLRLHLPQPPVQVQYEPSPAPS 60
QY 61 TTFSSNAPNFPDPDFVPPPPMPPSAQGLPCCIRPPPPNOMHPPFPVPCFPDM 120
DB 61 TTFSSNAPNFPDPDFVPPPPMPPSAQGLPCCIRPPPPNOMHPPFPVPCFPDM 120
QY 121 PPMPCPNPPVPVPGAPPQGTFFPMPPMPPSPMPPPPPPVMPQOVNYYPPGYSHNFPP 180
DB 121 PPMPCPNPPVPVPGAPPQGTFFPMPPMPPSPMPPPPPPVMPQOVNYYPPGYSHNFPP 180
QY 181 SFNSFQNNPSSFLPSANNSSSPHRLPPYLPKAPSERRSERLKHDDHRRDHSGR 240
DB 181 SFNSFQNNPSSFLPSANNSSSPHRLPPYLPKAPSERRSERLKHDDHRRDHSGR 240
QY 241 GERHSLDRERGRSDRRQDSRYSDYDRGRTPSRHESYERSRERERHRRDNR 300
DB 241 GERHSLDRERGRSDRRQDSRYSDYDRGRTPSRHESYERSRERERHRRDNR 300
QY 301 PSLESYKKEYKRSGRSYGLSVVPEPAGCTPBLPGEI IKNTDSWAPPLIIVNHSR 360
DB 301 PSLESYKKEYKRSGRSYGLSVVPEPAGCTPBLPGEI IKNTDSWAPPLIIVNHSR 360
QY 361 KRAWEEEEKDRWSDNQSGKDKNYTSIKKEPEETMPDKNEEBEELLKPWIRCTH 420
DB 361 KRAWEEEEKDRWSDNQSGKDKNYTSIKKEPEETMPDKNEEBEELLKPWIRCTH 420
QY 421 YSSDPMDQVGDSTVVGTSRLDYDKFEEELGSGQEKAKAAPPPWPKTKLDE 480
DB 421 YSSDPMDQVGDSTVVGTSRLDYDKFEEELGSGQEKAKAAPPPWPKTKLDE 480
QY 481 SESECSDESDTSCSSSDSEVDFVIAEIKRKAHPDLRDLHDELYNDPQWMDG 540
DB 481 SESECSDESDTSCSSSDSEVDFVIAEIKRKAHPDLRDLHDELYNDPQWMDG 540
QY 541 KAARTGIRHSIYPGEAIAKPCPMTNNAAGRLPHYRITVSPPTNFLTDRPTV 600
DB 541 KAARTGIRHSIYPGEAIAKPCPMTNNAAGRLPHYRITVSPPTNFLTDRPTV 600
QY 601 FEGFSMFAHAPLTNIDLCVKIRPNIDYTHFTEEMMPENFCVKGLELSLFL 660
DB 601 FEGFSMFAHAPLTNIDLCVKIRPNIDYTHFTEEMMPENFCVKGLELSLFL 660
QY 661 DNMLKGLFEDSPCCPRFHFMPRFRVFLPDGGKEVLSMHQIILLYLLRCS 720
DB 661 DNMLKGLFEDSPCCPRFHFMPRFRVFLPDGGKEVLSMHQIILLYLLRCS 720
QY 721 NMLQWEELEWQKYAECKGMIVTNPGTKPSSVRIQDLDRQFNPDVITPPI 780
DB 721 NMLQWEELEWQKYAECKGMIVTNPGTKPSSVRIQDLDRQFNPDVITPPI 780
QY 781 QLSYAGDPQYQKLWKSIVKRLHLLANSKPVKQTDKOKLAOREALOKIRK 840
DB 781 QLSYAGDPQYQKLWKSIVKRLHLLANSKPVKQTDKOKLAOREALOKIRK 840
QY 841 ELSQSQGFWTKGIRSDVCOHAMMLPVLTHTIRYHQCLMHLDKLIGYTF 900
DB 841 ELSQSQGFWTKGIRSDVCOHAMMLPVLTHTIRYHQCLMHLDKLIGYTF 900
QY 901 SHLNFQGNPDHARNLSNCGIRPQKYGDRKVHMMMRKKGINTLINIMSR 960
DB 901 SHLNFQGNPDHARNLSNCGIRPQKYGDRKVHMMMRKKGINTLINIMSR 960
QY 961 RINHNRLFLGDAVVEFLTSVHLVYLFPSLEBGGATVYRTAIVQNOHLAMAKKLELDP 1020
DB 961 RINHNRLFLGDAVVEFLTSVHLVYLFPSLEBGGATVYRTAIVQNOHLAMAKKLELDP 1020

QY 1021 FMLYAHGPDLCRSDLRHANCFEALIGAVYLEGSLAEAKQLFGRLLFNDPDLREVWLN 1080
DB 1021 FMLYAHGPDLCRSDLRHANCFEALIGAVYLEGSLAEAKQLFGRLLFNDPDLREVWLN 1080
QY 1081 YPLHPLQLQBPNTDRQLIETSPVLQKLTPEEAIGVIFTHVRLARAFRTLTGTFNHLTL 1140
DB 1081 YPLHPLQLQBPNTDRQLIETSPVLQKLTPEEAIGVIFTHVRLARAFRTLTGTFNHLTL 1140
QY 1141 GHNORMEFLGDSIMQLVATYLFIFHPDPHHEGHLTLRSSLVNNRTQAKVAEELGMQEYA 1200
DB 1141 GHNORMEFLGDSIMQLVATYLFIFHPDPHHEGHLTLRSSLVNNRTQAKVAEELGMQEYA 1200
QY 1201 ITNDKTRKPVGLRTKTLADLLESFIAALYTDKLEYVHTFMVCFPPRLKEFTLNQDWD 1260
DB 1201 ITNDKTRKPVGLRTKTLADLLESFIAALYTDKLEYVHTFMVCFPPRLKEFTLNQDWD 1260
QY 1261 PKSQLOQCCLTLTEGKEPDIPLYKTLQTPGSHARTYTVAVYFKGERICGKGPSIQQA 1320
DB 1261 PKSQLOQCCLTLTEGKEPDIPLYKTLQTPGSHARTYTVAVYFKGERICGKGPSIQQA 1320
QY 1321 EMGAAMDALEKYNFPQMAHQKRFGRKYRQELKEMRWERHQBREPDETDIKK 1374
DB 1321 EMGAAMDALEKYNFPQMAHQKRFGRKYRQELKEMRWERHQBREPDETDIKK 1374

RESULT 6
ABU63361
ID ABU63361 standard; protein; 1373 AA.
AC ABU63361;
XX
DT 18-SEP-2003 (first entry)
XX
DE Human double stranded RNase, RNase III.
XX
KW Human; enzyme; RNase III; double stranded RNase; RNA target;
KW gene silencing.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 18 /note= "Encoded by CGT"
FT Misc-difference 1211 /note= "Encoded by GCG"
FT Misc-difference 1345 /note= "Encoded by GAA"
XX
PN US2003044941-A1.
XX
PD 06-MAR-2003.
XX
PF 20-FEB-2002; 2002US-00079185.
XX
PR 06-JUN-1996; 96US-00659440.
PR 06-JUN-1997; 97US-00870608.
PR 07-JAN-2000; 2000US-00479783.
PR 06-JUL-2001; 2001US-00900425.
XX
PA (CROO/) CROOKE S T.
XX
PI Crooke ST;
XX
DR WPI: 2003-521756/49.
DR N-PSDB; ACD27526.
XX
PT Eliciting a modification of a selected RNA target in a cell, useful for
PT promoting inhibition of gene expression in a cell, comprises contacting
PT an RNA-like polynucleotide-RNA target duplex with a polypeptide having an
PT RNase III domain.
XX
PS Claim 37; Fig 1; 33pp; English.

XX The invention relates to eliciting a modification of a selected RNA
CC target in a cell comprises contacting an RNA-like polynucleotide-RNA
CC target duplex with a polypeptide comprising an RNase III domain. Also
CC included are promoting gene silencing in a cell, inhibiting the
CC expression of a gene in a cell comprising employing the method of cited
CC above, promoting inhibition of expression of a gene, a hybrid RNase III
CC (comprising at least one domain from a human RNase III and at least one
CC domain from an RNase III of an organism other than human) and a cell
CC having enhanced RNase III activity over an activity exhibited by a second
CC cell (where the second cell is not enriched with respect to the amount or
CC activity of RNase III polypeptide). The method is useful for eliciting a
CC modification of a selected RNA target in a cell, and for promoting
CC inhibition of expression of a gene in a cell. Compositions comprising
CC RNase III polypeptides or polynucleotides are useful for research,
CC biological and clinical purposes. The polynucleotides may be used in
CC defining the roles of RNase III and the interaction of human RNase III
CC and cellular RNA. Host cells can be used for the production of human
CC RNase III and for identifying agents, which increase or decrease levels
CC of expression or activity of human RNase III in the cell. The present
CC sequence represents human RNase III (a double stranded RNase)
XX
SQ Sequence 1373 AA;
Query Match 99.8%; Score 7483.5; D8 7; Length 1373;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1373; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MMQGNTRCHMSFHPGRGCGPRGCGHARGPSAPSRPNQLRLHLPQPPVQYQVEPPSAPS 60
DB 1 MMQGNTRCHMSFHPGRGCGPRGCGHARGPSAPSRPNQLRLHLPQPPVQYQVEPPSAPS 60
QY 61 TTFSNSPAPNLPDPDFVFPFPPMPSPSAQGLPPCPPIRPPFNHQRHPPVPVPCFPMP 120
DB 61 TTFSNSPAPNLPDPDFVFPFPPMPSPSAQGLPPCPPIRPPFNHQRHPPVPVPCFPMP 120
QY 121 PPPMPCNPPVPAGPPGQGTFFPMPPSPHPPPPPPVMPQVNTQYPPGYSHHPPPP 180
DB 121 PPPMPCNPPVPAGPPGQGTFFPMPPSPHPPPPPPVMPQVNTQYPPGYSHHPPPP 180
QY 181 SFNSFONNPFSSFLPSANNSSPHFRHLPPVPLPKAPSRSSPERLKHDDHRRDHSRGR 240
DB 181 SFNSFONNPFSSFLPSANNSSPHFRHLPPVPLPKAPSRSSPERLKHDDHRRDHSRGR 240
QY 241 GERHSLDRRGRSPDRRQDSRYSDYDRGTPSRHSYERSRERERHHRHNRRS 300
DB 241 GERHSLDRRGRSPDRRQDSRYSDYDRGTPSRHSYERSRERERHHRHNRRS 300
QY 301 PSLERSYKKEYKRSGRSYGLSVVPEPAGCTPBLPGBIINKTDSWAPPLAIIVNHRSPREK 360
DB 301 PSLERSYKKEYKRSGRSYGLSVVPEPAGCTPBLPGBIINKTDSWAPPLAIIVNHRSPREK 360
QY 361 KEARWEEKDRWSDNQSSGCKDKNYTSIKEKEPEETMPDKNEEEELLKPVVTRCTHSEN 420
DB 361 KEARWEEKDRWSDNQSSGCKDKNYTSIKEKEPEETMPDKNEEEELLKPVVTRCTHSEN 420
QY 421 YISSDPMDQVGDSTVVGTSRLRLDYDKFEEELGSRQEKAKAAPPPWPKTKLDEDLSS 480
DB 421 YISSDPMDQVGDSTVVGTSRLRLDYDKFEEELGSRQEKAKAAPPPWPKTKLDEDLSS 480
QY 481 SESECESDSDSTCSSSSDSEVDFVIAEIKRKAHPDRLHDELWYNDGQNDGPKCKCSA 540
DB 481 SESECESDSDSTCSSSSDSEVDFVIAEIKRKAHPDRLHDELWYNDGQNDGPKCKCSA 540
QY 541 KARRTGIRHSIYPGEAIAKPCRPMTNNAGRLPHYRTVSPPTNFLTDRPTVLEYDDHEVI 600
DB 541 KARRTGIRHSIYPGEAIAKPCRPMTNNAGRLPHYRTVSPPTNFLTDRPTVLEYDDHEVI 600
QY 601 FEGFSMFAHAPLTNIPLCVKIRFNIDYTHFTEEMWPNFVCVKGLELFLFLFRDILELY 660
DB 601 FEGFSMFAHAPLTNIPLCVKIRFNIDYTHFTEEMWPNFVCVKGLELFLFLFRDILELY 660
QY 661 DWNLKGPLFEDSPCCPRFHFMRFRVFLPDGCKEVLMSHQILLYLLRCSKALVPBEEIA 720

Db 179 ----- 178
QY 347 PLSIVNHRSPRKKARWEEKDRWSDNQSGDKNYTSIKKKEPEETMPDKNVEEEEE 406
Db 179 -----SRSPSRKKARWEEKDRWSDNQSGDKNYTSIKKKEPEETMPDKNVEEEEE 232
QY 407 LKPVWIRCTHSENYSSDDMDQVGDSTVVGTSRLDLYDKFEEELGSRQEKAKAAPPW 466
Db 233 LKPVWIRCTHSENYSSDDMDQVGDSTVVGTSRLDLYDKFEEELGSRQEKAKAAPPW 292
QY 467 EPKTKLDELSSSECSDESDSTCSSSDSEVPDVAIEIKRKAHPDRLHDELWYND 526
Db 293 EPKTKLDELSSSECSDESDSTCSSSDSEVPDVAIEIKRKAHPDRLHDELWYND 352
QY 527 PQQNDGPKCSAKARRTGIRHSIYPGEAIIKPCRPMTNNAAGRLPHYRITVSPPTNFLT 586
Db 353 PQQNDGPKCSAKARRTGIRHSIYPGEAIIKPCRPMTNNAAGRLPHYRITVSPPTNFLT 412
QY 587 DRETVIYDDHEVIFEGFSFAHAPLTNIPCLCKVIRFNIDYTHIFEEWMPNFCVKGLE 646
Db 413 DRETVIYDDHEVIFEGFSFAHAPLTNIPCLCKVIRFNIDYTHIFEEWMPNFCVKGLE 472
QY 647 LFSLFRLDILELYDNWNLKGPLFEDGPPCCPRFHFMPFRVFLPDGCKEVLMSHQILLYL 706
Db 473 LFSLFRLDILELYDNWNLKGPLFEDGPPCCPRFHFMPFRVFLPDGCKEVLMSHQILLYL 532
QY 707 LRCSKALVPEEETIANLQWEELEWQYAECKGMIVTNPCTKSSVRIDQLDREQPNPDV 766
Db 533 LRCSKALVPEEETIANLQWEELEWQYAECKGMIVTNPCTKSSVRIDQLDREQPNPDV 592
QY 767 ITPPIIVHFGIRPAQLSYAGDPQYQKLWKSIVKRLHLLANSPKVKQTDQKLAQREALQ 826
Db 593 ITPPIIVHFGIRPAQLSYAGDPQYQKLWKSIVKRLHLLANSPKVKQTDQKLAQREALQ 652
QY 827 KIRQKNTMRREVTVELSSQGFMTGIRSDVCOHAMMLPVLTHIRYHQCIMHLDKLIGYT 886
Db 653 KIRQKNTMRREVTVELSSQGFMTGIRSDVCOHAMMLPVLTHIRYHQCIMHLDKLIGYT 712
QY 887 FQDRCLLQALWTHPSHLHFGNPDHARNSLSCGIRQPKYQDRKVHMHMRKKGINTLI 946
Db 713 FQDRCLLQALWTHPSHLHFGNPDHARNSLSCGIRQPKYQDRKVHMHMRKKGINTLI 772
QY 947 NIMSLRGQDDPTPSRINHNRLERFLGDVAVVEFLTSVHLIYLPSPLEGGIATYRTAIVQN 1006
Db 773 NIMSLRGQDDPTPSRINHNRLERFLGDVAVVEFLTSVHLIYLPSPLEGGIATYRTAIVQN 832
QY 1007 QHLAMLAKKLELDPFMYAHGPDLCRESDLRHAWANCFEALIGAVYLEGSLREAKOLFGR 1066
Db 833 QHLAMLAKKLELDPFMYAHGPDLCRESDLRHAWANCFEALIGAVYLEGSLREAKOLFGR 892
QY 1067 LLFNDPDLREVWNLNYPHPLQLQEPNTDQLIETSPVLQKLTFFEBEAIQVIFTHVRLAR 1126
Db 893 LLFNDPDLREVWNLNYPHPLQLQEPNTDQLIETSPVLQKLTFFEBEAIQVIFTHVRLAR 952
QY 1127 APTLRTVGFNHLTLGHNQRMFEGDSIMQIVATEYLFPIHPDDHHEGLTLRLSSLVNNT 1186
Db 953 APTLRTVGFNHLTLGHNQRMFEGDSIMQIVATEYLFPIHPDDHHEGLTLRLSSLVNNT 1012
QY 1187 QAKVAELGNGQVATINDKTKRPVGLTKTLADLLESFTAAALYTDKOLEVHTFMNVCF 1246
Db 1013 QAKVAELGNGQVATINDKTKRPVGLTKTLADLLESFTAAALYTDKOLEVHTFMNVCF 1072
QY 1247 PRUKETILQDNDPKSQOCCCLTLRTEGKEDIPLXYKLTQVGPSHARTYVAVYFKG 1306
Db 1073 PRUKETILQDNDPKSQOCCCLTLRTEGKEDIPLXYKLTQVGPSHARTYVAVYFKG 1132
QY 1307 ERIGCGKGPSIQAEAGMADALEKYNFPQMAHQKFIKRYQKELKMRWEREHQEREP 1366
Db 1133 ERIGCGKGPSIQAEAGMADALEKYNFPQMAHQKFIKRYQKELKMRWEREHQEREP 1192
QY 1367 DETEDIKK 1374
|||||

Db 1193 DETEDIKK 1200
RESULT 8
ABU08060
ID ABU08060 standard; protein; 1374 AA.
XX
AC ABU08060;
XX
DT 16-MAY-2003 (first entry)
XX
Human RNase III protein.
XX
Human; enzyme; RNase III; ribonuclease III; endoribonuclease;
KW pre-ribosomal RNA; pre-rRNA; small molecular weight nuclear RNA; snRNA;
KW small molecular weight nuclear RNA; snRNA; mRNA degradation;
KW antisense therapy; RNA interference; RNAi; gene therapy;
KW infectious agent; prophylaxis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
Region 161..168
FT /label= Alpha_helix_1
Region 181..189
FT /label= Beta_sheet_1
Region 196..202
FT /label= Beta_sheet_2
Region 207..214
FT /label= Beta_sheet_3
Region 215..235
FT /label= Alpha_helix_2
XX
PN US2002164601-A1.
XX
07-NOV-2002.
XX
06-JUL-2001; 2001US-00900425.
XX
06-JUN-1996; 96US-00659440.
PR 06-JUN-1997; 97US-00870608.
PR 07-JAN-2000; 2000US-00479783.
XX
(WUHH/) WU H.
PA (CROO/) CROOKE S T.
XX
Wu H, Crooke ST;
PI
XX
WPI; 2003-328390/31.
DR
XX
New human RNase polypeptide, useful for screening antisense
PT oligonucleotides for therapy of disorders associated with RNase III
PT expression or activity, or for evaluating the efficacy of an antisense
PT therapy.
XX
Claim 3; Fig 1; 17pp; English.
PS
XX
The invention discloses an isolated human ribonuclease III (RNase III)
CC polypeptide, and the nucleic acid encoding it. RNase III is an
CC endoribonuclease that cleaves double stranded RNA. All RNase III species
CC contain an RNase III signature sequence. RNase III has been reported to
CC be involved in the processing of pre-ribosomal RNA (pre-rRNA), small
CC molecular weight nuclear RNAs (snRNAs) and small molecular weight
CC nuclear RNAs (snRNAs), as well as the degradation of some mRNA
CC species. Also disclosed is an antibody targeted to the human RNase III
CC polypeptide, an antisense compound 8 50 nucleobases in length, which is
CC targeted to the nucleic acid encoding human RNase III polypeptide, and
CC methods for inhibiting human RNase III expression, or activity, in a cell
CC or tissue, identifying agents that increase or decrease the activity or
CC levels of the human RNase III polypeptide in a host cell, screening
CC oligonucleotides to identify effective antisense oligonucleotides for
CC inhibition of expression of a selected target protein, prognosticating
CC efficacy of antisense therapy of a selected disease, eliciting cleavage

CC	of a selected cellular RNA target and promoting RNA interference (RNAi)									
CC	in a cell. The RNase III polypeptide, the polynucleotide encoding it and									
CC	the antisense oligonucleotides, are useful for gene therapy (e.g. for									
CC	treating a disease or disorder associated with RNase III expression or									
CC	activity, or associated with an infectious agent), prophylaxis or as									
CC	research reagents. The sequence presented is the human RNase III protein									
XX										
XX										
SQ	Sequence 1374 AA;									
	Query Match	80.8%;	Score	6062;	DB	6;	Length	1374;		
	Best Local Similarity	100.0%;	Pred. No.	0;						
	Matches 1101;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
QY	1	MMQGNCHRNSTFPGRCGRGGHGHGAPSFQPNQLRLHLPQPPVQYQVEPPSAPS	60							
DB	274	MMQGNCHRNSTFPGRCGRGGHGHGAPSFQPNQLRLHLPQPPVQYQVEPPSAPS	333							
QY	61	TTFSNSPAPNPLPRDFVFPFPPMPPSAQCPLPPIRPPFNHQRHPFPVPPCFPPM	120							
DB	334	TTFSNSPAPNPLPRDFVFPFPPMPPSAQCPLPPIRPPFNHQRHPFPVPPCFPPM	393							
QY	121	PPMPCPNPVPVPGAPPGQGTFFPMPPSPSMHPHPPPPVMPQVNTQYPPGYSHHNPFP	180							
DB	394	PPMPCPNPVPVPGAPPGQGTFFPMPPSPSMHPHPPPPVMPQVNTQYPPGYSHHNPFP	453							
QY	181	SFNSFQNPSSFLPSANSSSPHRLPPYPLKAPSERRSPERLKHDDHRRDHSR	240							
DB	454	SFNSFQNPSSFLPSANSSSPHRLPPYPLKAPSERRSPERLKHDDHRRDHSR	513							
QY	241	GERHSLDRRGRSPDRRQDSRYSDYDRGTGSRHSYERSRERERHRHRDNR	300							
DB	514	GERHSLDRRGRSPDRRQDSRYSDYDRGTGSRHSYERSRERERHRHRDNR	573							
QY	301	PSLSRYKYEKRSYGLSVVPEPAGCTPELPGIINKTDSWAPPLEIVNHRSPREK	360							
DB	574	PSLSRYKYEKRSYGLSVVPEPAGCTPELPGIINKTDSWAPPLEIVNHRSPREK	633							
QY	361	KRARWEEKDRWDNQSGDKDKNYTSIKKEPETPMDKNEEEELLKPVWIRCTHSEN	420							
DB	634	KRARWEEKDRWDNQSGDKDKNYTSIKKEPETPMDKNEEEELLKPVWIRCTHSEN	693							
QY	421	YSSDPMQVGDSTVGTSLRLDYKFEELSGROKAKAAPPPWPEPKTKLDELESS	480							
DB	694	YSSDPMQVGDSTVGTSLRLDYKFEELSGROKAKAAPPPWPEPKTKLDELESS	753							
QY	481	SESECEDESDTSCSSSDSEVDFVIAIKRKAHPDRHLDLWYNDPGQNDGPKCKSA	540							
DB	754	SESECEDESDTSCSSSDSEVDFVIAIKRKAHPDRHLDLWYNDPGQNDGPKCKSA	813							
QY	541	KARRTGIRHSIYGEAEIKPCRPMTNAGRLFYRITVSPPTNFLTDRPTVIEYDDHEYI	600							
DB	814	KARRTGIRHSIYGEAEIKPCRPMTNAGRLFYRITVSPPTNFLTDRPTVIEYDDHEYI	873							
QY	601	FEGFSFAHAPLNTIPLCKVIRNIDYTHFIREMPENFCVKGLEFLSLFRDILELY	660							
DB	874	FEGFSFAHAPLNTIPLCKVIRNIDYTHFIREMPENFCVKGLEFLSLFRDILELY	933							
QY	661	DMNLKGLFEDSPCCPRFHFMPFRVFLPDGKGVLSMHQIILLYLLRCSKALVPBEEIA	720							
DB	934	DMNLKGLFEDSPCCPRFHFMPFRVFLPDGKGVLSMHQIILLYLLRCSKALVPBEEIA	993							
QY	721	NMLQWEELEWQKVAECKGMIVTNPQKPSVRIQDLDRQFNPDPVTTFPIIVHFGIRPA	780							
DB	994	NMLQWEELEWQKVAECKGMIVTNPQKPSVRIQDLDRQFNPDPVTTFPIIVHFGIRPA	1053							
QY	781	QLSVAGDPQYQKWLKSVVLRHLLANSFKVQTDKQKLAOREALQKIROKNTWRRVTV	840							
DB	1054	QLSVAGDPQYQKWLKSVVLRHLLANSFKVQTDKQKLAOREALQKIROKNTWRRVTV	1113							
QY	841	ELSSQGFWKTGIRSDVQCQHAMMLPVLTHIRYHQCLMHLDKLIGYTPQDRCLLQAMTHP	900							
DB	1114	ELSSQGFWKTGIRSDVQCQHAMMLPVLTHIRYHQCLMHLDKLIGYTPQDRCLLQAMTHP	1173							

QY	901	SHLNFNMNPDHARNSLNSCGIRQPKYQDRKVHMHMRKKGINTLINIMSRGQDDPTPS	960
DB	1174	SHLNFNMNPDHARNSLNSCGIRQPKYQDRKVHMHMRKKGINTLINIMSRGQDDPTPS	1233
QY	961	RINHNRLBFLGDGVVEFLTSVHLIYFLPSLBEGGLATYRTAIVQNHMLAKKLELDP	1020
DB	1234	RINHNRLBFLGDGVVEFLTSVHLIYFLPSLBEGGLATYRTAIVQNHMLAKKLELDP	1293
QY	1021	FMLYAHGPDLCRESDLRHAWANCFEALIGAVYLEGSLEBAKOLFGRLLFNDPDLREVWLN	1080
DB	1294	FMLYAHGPDLCRESDLRHAWANCFEALIGAVYLEGSLEBAKOLFGRLLFNDPDLREVWLN	1353
QY	1081	YPLHPLQLQEPNTDROLIETS 1101	
DB	1354	YPLHPLQLQEPNTDROLIETS 1374	
RESULT 9			
ID	AAB92635		
AA	AAB92635	standard; protein; 769 AA.	
XX	AAB92635;		
XX	XX		
DT	26-JUN-2001	(first entry)	
XX	XX		
DE	Human protein sequence SEQ ID NO:10949.		
XX	Human; primer; detection; diagnosis; antisense therapy; gene therapy.		
XX	Homo sapiens.		
OS	Homo sapiens.		
PN	EP1074617-A2.		
XX	XX		
PD	07-FEB-2001.		
XX	XX		
PF	28-JUL-2000; 2000EP-00116126.		
XX	XX		
PR	29-JUL-1999; 99JP-00248036.		
PR	27-AUG-1999; 99JP-00300253.		
PR	11-JAN-2000; 2000JP-00118776.		
PR	02-MAY-2000; 2000JP-00183767.		
PR	09-JUN-2000; 2000JP-00241899.		
XX	XX		
PA	(HELI-) HELIX RES INST.		
XX	XX		
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
XX	WPI; 2001-318749/34.		
DR	XX		
XX	XX		
PT	Primer sets for synthesizing polynucleotides, particularly the 5602 full-		
PT	length cDNAs defined in the specification, and for the detection and/or		
PT	diagnosis of the abnormality of the proteins encoded by the full-length		
PT	cDNAs.		
XX	XX		
PS	Claim 8; SEQ ID NO 10949; 2537pp + Sequence Listing; English.		
XX	XX		
CC	The present invention describes primer sets for synthesising 5602 full-		
CC	length cDNAs defined in the specification. Where a primer set comprises:		
CC	(a) an oligo-dT primer and an oligonucleotide complementary to the		
CC	complementary strand of a polynucleotide which comprises one of the 5602		
CC	nucleotide sequences defined in the specification, where the		
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination		
CC	of an oligonucleotide comprising a sequence complementary to the		
CC	complementary strand of a polynucleotide which comprises a 5'-end		
CC	sequence and an oligonucleotide comprising a sequence complementary to a		
CC	polynucleotide which comprises a 3'-end sequence, where the		
CC	oligonucleotide comprises at least 15 nucleotides and the combination of		
CC	the 5'-end sequence/3'-end sequence is selected from those defined in the		
CC	specification. The primer sets can be used in antisense therapy and in		
CC	gene therapy. The primers are useful for synthesising polynucleotides,		
CC	particularly full-length cDNAs. The primers are also useful for the		
CC	detection and/or diagnosis of the abnormality of the proteins encoded by		

CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 769 AA;

Query Match 54.3%; Score 4071; DB 4; Length 769;
Best Local Similarity 99.5%; Pred. No. 4.2e-280;
Matches 765; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 606 MFAHAPLTNIPCKVIRFNIDYTHFTIEEMMPNFCVKGLELSFLFRDILSLYDNLK 665
Db 1 MFAHAPLTNIPCKVIRFNIDYTHFTIEEMMPNFCVKGLELSFLFRDILSLYDNLK 60
QY 666 GPLPEPSPCCPRPFHMPFRVRLPDGKGVLSMHQILLYLLRCSKALVPEEIRIANLQW 725
Db 61 GPLPEPSPCCPRPFHMPFRVRLPDGKGVLSMHQILLYLLRCSKALVPEEIRIANLQW 120
QY 726 EELEWKQYAECKGMIVTNGTTPSSVRIDQLDREQFNPDVITPPIIVHFGIRPAQLSYA 785
Db 121 EELEWKQYAECKGMIVTNGTTPSSVRIDQLDREQFNPDVITPPIIVHFGIRPAQLSYA 180
QY 786 GDPQYOKLWKSYVKLRHLLANSKVKQTDKQKLAOREALQKIROKNTMRREVTVLSSQ 845
Db 181 GDPQYOKLWKSYVKLRHLLANSKVKQTDKQKLAOREALQKIROKNTMRREVTVLSSQ 240
QY 846 GFWKGTGIRSDVCOHAMWLPVTHIRYHQCMLHDLKLIYTFQDRCCLQLAMTHPSHLLN 905
Db 241 GFWKGTGIRSDVCOHAMWLPVTHIRYHQCMLHDLKLIYTFQDRCCLQLAMTHPSHLLN 300
QY 906 FGNPDPHARNSLNCGIROPKYGDVKVHHMHRKKGINTLINMSRLGQDDPTPSRINHN 965
Db 301 FGNPDPHARNSLNCGIROPKYGDVKVHHMHRKKGINTLINMSRLGQDDPTPSRINHN 360
QY 966 ERLEFLGDAVVEFLTSHVLYLPPSLEEGGLATYRTAIVQNHMLAKKLELDPFMYA 1025
Db 361 ERLEFLGDAVVEFLTSHVLYLPPSLEEGGLATYRTAIVQNHMLAKKLELDPFMYA 420
QY 1026 HGPDLGRESLDRHAMCNCFALIGAVYLEGSLEAKQLFGRLLFNDPDLREVWLNYPHP 1085
Db 421 HGPDLGRESLDRHAMCNCFALIGAVYLEGSLEAKQLFGRLLFNDPDLREVWLNYPHP 480
QY 1086 LQIQEENTDQLTETSPVLQKLEFEAEIGVITFHVRLARAFRTLVGFNHLTLGHNR 1145
Db 481 LQIQEENTDQLTETSPVLQKLEFEAEIGVITFHVRLARAFRTLVGFNHLTLGHNR 540
QY 1146 MEFLGDSIMQLVATEYLFIHFPDHEGHLTLRSSLVNNTQAKVABELGMQSYAITNDK 1205
Db 541 MEFLGDSIMQLVATEYLFIHFPDHEGHLTLRSSLVNNTQAKVABELGMQSYAITNDK 600
QY 1206 TKRPVGLRTKTLADLLESFIAALYTDKLELYVTFMNVCFPPRLKFEILNQDNDPKSQL 1265
Db 601 TKRPVGLRTKTLADLLESFIAALYTDKLELYVTFMNVCFPPRLKFEILNQDNDPKSQL 660
QY 1266 QOCLTLRTGKGPDIPLYKTLQTVGFSHARTTVAVYFGERIGCKGKPSIOQAEWGAA 1325
Db 661 QOCLTLRTGKGPDIPLYKTLQTVGFSHARTTVAVYFGERIGCKGKPSIOQAEWGAA 720
QY 1326 MDALKYNFPQMAHQKRFGRKYRQELKEMRWEREHQERPEDETIKK 1374
Db 721 MDALKYNFPQMAHQKRFGRKYRQELKEMRWEREHQERPEDETIKK 769

RESULT 10
ABB58539
ID ABB58539 standard; protein; 1327 AA.
XX
AC ABB58539;
XX
DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 2409.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
KW Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US009231.
PF
XX 23-MAR-2000; 2000US-0191637P.
PR
XX 11-JUL-2000; 2000US-00614150.
PR
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR
XX N-PSDB; ABL02642.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
PT
XX Disclosure; SEQ ID NO 2409; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ffp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1327 AA;

Query Match 39.5%; Score 2963; DB 4; Length 1327;
Best Local Similarity 45.6%; Pred. No. 4.7e-201;
Matches 621; Conservative 213; Mismatches 327; Indels 200; Gaps 32;

QY 90 QGPLPCPIRPPPPNHQMRHPPVPFCFPMPMPMPCPN-NPPVPGAP-----P 137
Db 3 QPLPLPPPPVQPA-----PPPPPPPEEDLSPPGVGVPVSHNYSNESHQ 46
QY 138 GQGTFFPMPPSPMPPPPPPVMPVMPQVNYQYPPGY-----SHNFP 179
Db 47 SSKSLDYVVPETAPYASS---VPSYDVPQOPAYGYEGVAYNEQAQYGGQSHVQYQY 103
QY 180 PPSNFPQNNPSPFLPSANNSSPHFRLPPYPL-----PKAPSRERRSPERLKHVDHHRD 235
Db 104 PA-----SGSSFLYES-----YKYPDRYPAYSSNYRPPSERQ-----RYTS 139
QY 236 HSHGRCGERHSLDRRERGSPDRRRQDSYRSYDRGRTPSRHSYRSEREREHHR 295
Db 140 NSSSQYHYHYP-----GYSSGR-----RYEQRHQ-----EHRQODSYAHPRHGHY 183
QY 296 DNRSPSLERSYKKEKRSYGLSWPWPAGCTPELPGEIYKNTDSSWAPPLEIVNHR 355
Db 184 AHRQAKSGOHGY---YGSARN-----QVSDDYSPRGHERERN 219
QY 356 PREKRA--RWEEKOR-----WSDNQSGKKNYTSIKEKPEETMPDKNEEBELK 409
Db 220 ETLEKTRAKPKVETERDRLRLQWCSNFC-----EKDEDYVKKNALSEADAPV 267
QY 410 FWIRCTSHENYSSDPMQVGDSTVGTSLRLDLTKFEELGSRQEKAKARPWP 469

KW clinical purpose; cellular interaction.
XX Homo sapiens.
OS US2004126867-A1.
XX 01-JUL-2004.
XX
XX 09-FEB-2004; 2004US-00774974.
XX
XX 06-JUL-2001; 2001US-00900425.
XX
XX (CROO/) CROOKE S T.
XX (WUHH/) WU H.
XX
XX Crooke ST, Wu H;
XX
XX WPI; 2004-516913/49.
XX
XX New isolated nucleic acid molecule encoding human RNase III, useful for
PT research, biological, or clinical purposes, e.g. defining the roles of
PT RNase III and the interaction of human RNase III and cellular RNA.
XX
XX Example 9; SEQ ID NO 37; 31dp; English.
XX
XX The invention relates to human ribonuclease III (RNase III) and its
CC corresponding nucleic acid sequence. The polynucleotide sequence of the
CC invention is useful for research, biological and clinical purposes. It is
CC useful in defining the roles of RNase III and the interaction of human
CC RNase III and cellular RNA. The present sequence is human RNase III-like
CC domain protein.
XX
XX SQ Sequence 466 AA;

Query Match 32.8%; Score 2463; DB 8; Length 466;
Best Local Similarity 100.0%; Pred. No. 4e-166;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 909 NPDHARSLNCSGIRPKYGDVKVHHMMKKGKINTLIMSLRGQDDPPPSININERL 968
Db 1 NPDHARSLNCSGIRPKYGDVKVHHMMKKGKINTLIMSLRGQDDPPPSININERL 60

QY 969 EFLGDVAVVEPLTSVHLYLPPSLEEGLATYRTAIVQNHSLAMAKKLEDPFMYAHGP 1028
Db 61 EFLGDVAVVEPLTSVHLYLPPSLEEGLATYRTAIVQNHSLAMAKKLEDPFMYAHGP 120

QY 1029 DLCRSDLRHAMANCFEALIGAVYLEGSLEAKQLFGRLLFNDPDLREVWLNYPHLPLQL 1088
Db 121 DLCRSDLRHAMANCFEALIGAVYLEGSLEAKQLFGRLLFNDPDLREVWLNYPHLPLQL 180

QY 1089 QEPNDRQLIETSPVLQKLTPEFEAIGVIFTHVRLRLARAFPLRTVGFNHLTLGHNORMEP 1148
Db 181 QEPNDRQLIETSPVLQKLTPEFEAIGVIFTHVRLRLARAFPLRTVGFNHLTLGHNORMEP 240

QY 1149 LGSIMQLVATEYLFTHFPDHHGHLTLRLSSLVNNTQAKVAEELGMOEYAITNDKTKR 1208
Db 241 LGSIMQLVATEYLFTHFPDHHGHLTLRLSSLVNNTQAKVAEELGMOEYAITNDKTKR 300

QY 1209 PVGLRTKTLADLLESFIAALYTDKLEYVHTFMNVCFFPRLKBFILNQDWNPKSQLOQC 1268
Db 301 PVGLRTKTLADLLESFIAALYTDKLEYVHTFMNVCFFPRLKBFILNQDWNPKSQLOQC 360

QY 1269 CLTLRTGKEPDIPLYKTLQTVGFSHARTYTVAYFKGERIGCGKGPSIQQAEMGAAMD 1328
Db 361 CLTLRTGKEPDIPLYKTLQTVGFSHARTYTVAYFKGERIGCGKGPSIQQAEMGAAMD 420

QY 1329 LEKNYFQMAHQRFGRKRYOELKEMRWEREHOEPEDETIKK 1374
Db 421 LEKNYFQMAHQRFGRKRYOELKEMRWEREHOEPEDETIKK 466

RESULT 14
AAU20587

AAU20587 standard; protein; 378 AA.
AAU20587;
04-DEC-2001 (first entry)
Human secreted protein, Seq ID No 579.
Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina;
rheumatoid arthritis; antiarteriosclerotic; cardiac; vascular;
cerebroprotective; thrombolytic; antimicrobial; ophthalmological;
cytostatic; Alzheimer's disease; Parkinson's disease; human; cancer;
multiple sclerosis; cancer; hyperproliferative disorder; infection;
Gaucher's disease; neurological disease; cerebrovascular disorder;
thrombosis; wound healing.
Homo sapiens.
WO200155326-A2.
02-AUG-2001.
17-JAN-2001; 2001WO-US001347.
31-JAN-2000; 2000US-0179065P.
04-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0190076P.
18-APR-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0205515P.
07-JUN-2000; 2000US-0209467P.
28-JUN-2000; 2000US-0214886P.
30-JUN-2000; 2000US-0215135P.
07-JUL-2000; 2000US-0216647P.
07-JUL-2000; 2000US-0216880P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217496P.
14-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0220963P.
26-JUL-2000; 2000US-0220964P.
14-AUG-2000; 2000US-0224518P.
14-AUG-2000; 2000US-0224519P.
14-AUG-2000; 2000US-0225213P.
14-AUG-2000; 2000US-0225214P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225267P.
14-AUG-2000; 2000US-0225268P.
14-AUG-2000; 2000US-0225270P.
14-AUG-2000; 2000US-0225447P.
14-AUG-2000; 2000US-0225757P.
14-AUG-2000; 2000US-0225758P.
14-AUG-2000; 2000US-0225759P.
18-AUG-2000; 2000US-0226279P.
22-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-0226868P.
22-AUG-2000; 2000US-0227182P.
23-AUG-2000; 2000US-0227009P.
30-AUG-2000; 2000US-0228924P.
01-SEP-2000; 2000US-0229287P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229345P.
05-SEP-2000; 2000US-0229509P.
05-SEP-2000; 2000US-0229513P.
06-SEP-2000; 2000US-0230437P.
06-SEP-2000; 2000US-0230438P.
08-SEP-2000; 2000US-0231242P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232337P.
PR 14-SEP-2000; 2000US-0232338P.
PR 14-SEP-2000; 2000US-0232339P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 23-SEP-2000; 2000US-0234937P.
PR 25-SEP-2000; 2000US-0234938P.
PR 26-SEP-2000; 2000US-0234984P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239377P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
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PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
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PR 17-NOV-2000; 2000US-0249299P.
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PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 03-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX
XX WPI; 2001-451931/48.
DR N-PSDB; AAS33296.
DR
XX
PT New nucleic acids and polypeptides, useful for diagnosing, preventing or
XX treating medical conditions.
PS Claim 11; SEQ ID NO 579; 753pp; English.
XX
CC The invention relates to novel isolated nucleic acid molecules (I)
CC encoding human secreted proteins (II). (I) and (II) are used to prevent,
CC treat or ameliorate a medical condition in e.g. humans, mice, rabbits,
CC goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in
CC the prevention, treatment and diagnosis of diseases associated with
CC inappropriate expression of secreted proteins. (I) and complementary
CC sequences may also be used as DNA probes in diagnostic assays (e.g.
CC polymerase chain reactions (PCR)) to detect and quantitate the presence
CC of similar nucleic acid sequences in samples, and so which patients may
CC be in need of restorative therapy. (II) may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of the secreted
CC proteins. The anti-(II) antibodies and antagonists may also be used to
CC down regulate expression and activity of (II). The anti-(II) antibodies
CC may also be used as diagnostic agents for detecting the presence of (II)
CC in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The
CC disorders include for example: immune/autoimmune diseases (e.g. HIV
CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
CC Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
CC cerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and
CC thrombosis), infections caused by bacteria, viruses and fungi and ocular
CC disorders (e.g. corneal infections). (I) and (II), agonists, antagonists
CC and antibodies can also be used to promote wound healing, maintain organs
CC before transplantation, and support cell culture of primary tissues.

Query Match 26.1%; Score 1961; DB 4; Length 378;
Best Local Similarity 98.9%; Pred. No. 1.4e-130;
Matches 374; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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QY 1057 LREAKOLFGRLLFNDFNDPDLREVWLNYPHLPLOQEPNTDROLIETSPVLOKLTFFERAGV 1116
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DB 121 IFTHVELLARAFPTLRTVGFNHLTLGHNRMEFLGDSIMOLVATEYLFIFHPDHEGHJTL 180
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Db 181 LRSSLVNRRTQAKVAEELGMEQVAITNDKTRPVALRTKTLADLLRSFIAALYIDKOLEY 240
Qy 1237 VHTFMNVCFPRUKBPIILNQDWDNPKSLOQCCCLTLRTGKEDPIDLYKTLQTVGSPSHAR 1296
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Db 301 TYTVAVYFVGERIGCGKGPSIQAEAGMAAMDALEKYNFPMOAHQKRFPIGRKYRQELKEWR 360
Qy 1357 WEREHQEREPEDETIKK 1374
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ID AAU211744 standard; protein; 378 AA.
AC AAU211744;
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DT 04-DEC-2001 (first entry)
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DE Novel human neoplastic disease associated polypeptide #177.
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KW Human; neoplastic disease associated polypeptide; cancer;
KW hyperproliferative disorder; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW neuroprotective; cytostatic; anti inflammatory; vasotropic.
XX
OS Homo sapiens.
XX
PN WO200155163-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US0001358.
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PR 31-JAN-2000; 2000US-0179065P.
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XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPI: 2001-465558/50.	
DR	N-PSDB; AAS34943.	
XX		
PT	Novel polypeptides and polynucleotides useful as diagnostic reagents to	
PT	diagnose diseases or disorders associated with aberrant expression or	
PT	activity of polypeptides, and for treating cancers, rheumatoid arthritis.	
XX		
PS	Claim 11; SEQ ID NO 471; 687pp; English.	
XX		
CC	The present invention relates to the isolation of novel human neoplastic	
CC	disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA	
CC	sequences encoding for these polypeptides. The sequences of the invention	
CC	are useful in the diagnosis, treatment, prevention and/or prognosis of	
CC	disorders involving neoplastic disease such as hyperproliferative	
CC	disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem	
CC	glioma, adult liver cancer, childhood cerebellar astrocytoma, or	
CC	Hodgkin's lymphoma). The sequences of the invention may also be useful	
CC	for treating other disorders such as neural disorders, immune system	
CC	disorders, muscular disorders, reproductive disorders, gastrointestinal	
CC	disorders, pulmonary disorders, cardiovascular disorders and renal	
CC	disorders. The polynucleotide sequences of the invention are also useful	
CC	in gene therapy. AAU21568-AAU21851 represent the novel human neoplastic	
CC	disease associated polypeptides of the invention. Note: The sequence data	
CC	for this patent did not form part of the printed specification, but was	
CC	obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 378 AA;	

Query Match	26.1%	Score 1961;	DB 4;	Length 378;
Best Local Similarity	98.9%	Pred. No. 1.4e-130;		
Matches 374;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
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QY	1057	LEBAKQLFGRLLFNDPDLREVWLNYPFLPQLQEPNTDRLQIETSPVLQKLTFFEEAIGV	1116	

Db	61	LEBAKQLFGRLLFNDPDLREVWLNYPFLPQLQEPNTDRLQIETSPVLQKLTFFEEAIGV	120
QY	1117	IFTHVRLARAFTLRTVGFNHLTLGHNQRMFGLGDSIMQLVATEYLFIHPPDHHEGHLTL	1176
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QY	1177	LRSSLVNNRTQAKVAEELGMQEVATINDKTKRPVGLRTKTLADLLESFIAALYTDKLEY	1236
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QY	1237	VHTFMNVCFPPRLKGFILNQDNDPKSQQQCCCLTLRTGKESPDIPLYKTLQTVGFSHAR	1296
Db	241	VHTFMNVCFPPRLKGFILNQDNDPKSQQQCCCLTLRTGKESPDIPLYKTLQTVGFSHAR	300
QY	1297	TYTVAVYFKGERIGCGKGPSIQQAENGAAAMDALEKYNFPQMAHQKRFIQRKYQELKEMR	1356
Db	301	TYTVAVYFKGERIGCGKGPSIQQAENGAAAMDALEKYNFPQMAHQKRFIQRKYQELKEMR	360
QY	1357	WEREHQEREPEDETIKK	1374
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 24, 2005, 00:35:55 ; Search time 29 Seconds
(without alignments)
4558.684 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	558	7.4	682	2 T21420	hypothetical prote
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4	315	4.2	249	2 B69693	ribonuclease III (
5	307.5	4.1	229	2 A81300	ribonuclease III h
6	300	4.0	229	2 A81572	ribonuclease III h
7	293	3.9	1560	2 T42727	proliferation pote
8	285.5	3.8	225	2 B82073	ribonuclease III v
9	282	3.8	263	2 A83961	ribonuclease III r
10	281.5	3.8	232	2 P98012	ribonuclease III (
11	279.5	3.7	232	2 H95144	ribonuclease III (
12	276	3.7	948	2 A57640	retinoblastoma bin
13	275	3.7	760	2 T06291	extensin homolog T
14	274.5	3.7	1531	2 T48946	hypothetical prote
15	273.5	3.6	1006	2 G86292	hypothetical prote
16	273	3.6	891	2 G84693	probable proline-r
17	271.5	3.6	620	2 S06733	hydroxyproline-ric
18	270	3.6	226	2 H84959	ribonuclease III (
19	268.5	3.6	231	2 B86725	ribonuclease III (
20	267	3.6	224	2 A81260	ribonuclease III (
21	267	3.6	243	2 D89896	RNAse III (importe
22	267	3.6	998	2 T30930	hypothetical prote
23	265.5	3.5	1002	2 T43236	carboxypeptidase C
24	262	3.5	226	1 NREC3	ribonuclease III (
25	262	3.5	226	2 F85902	RNAse III, ds RNA
26	262	3.5	226	2 A91058	RNAse III (importe
27	259	3.5	322	2 S25299	extensin precursor
28	258	3.4	231	2 S76204	hypothetical prote
29	257.5	3.4	272	2 T35656	ribonuclease III -

30	256	3.4	246	2 H70187	ribonuclease III (
31	255.5	3.4	1638	2 A42091	transcription acti
32	255	3.4	226	2 AC0829	ribonuclease III (
33	254	3.4	1611	2 T38236	hypothetical prote
34	253.5	3.4	368	2 C29356	hydroxyproline-ric
35	253.5	3.4	1048	2 T31425	C-terminal domain-
36	252	3.4	226	2 AF0331	ribonuclease III (
37	251.5	3.4	240	2 P64602	ribonuclease III -
38	251.5	3.4	1201	2 G86441	unknown protein (i
39	250.5	3.3	727	2 C84534	hypothetical prote
40	249	3.3	225	2 T09964	extensin CYC15 pre
41	249	3.3	907	2 E96636	hypothetical prote
42	249	3.3	1877	2 T21861	hypothetical prote
43	245	3.3	230	2 G97115	dsRNA-specific rib
44	244.5	3.3	489	2 T11622	extensin class 1 p
45	243.5	3.2	708	2 D96711	hypothetical prote

ALIGNMENTS

RESULT 1

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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21419
R;Lightning, J.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19419
A;Accession: T21419
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-412 <WIL>
A;Cross-references: UNIPARC:UPI000017B936; EMBL:Z81070; PIDN:CA803005.1; GSPDB:GN000019; (C
A;Experimental source: clone F26E4
C;Genetics:
A;Gene: CESP:F26E4.13
A;Map position: 1
A;Introns: 359/2; 400/3

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								7;
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QY	1183	NNRTQAKVAEELGMQBYAITNDKTRPV---GLRTKTLADLLESFTAAALYTDKLEVHT	1239					
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T42727
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C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42727
R:Witte, M.M.; Scott, R.E.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z22246
A:Accession: T42727
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1560 <WIT>
A:Cross-references: UNIPROT:P97868; UNIPARC:UPI0000028767; EMBL:U83913; NID:g3858884; P1
A:Experimental source: strain Balb/C
C:Genetics:
A:Gene: P2P-R
C:Function:
A:Description: involved in hnRNP association and Rb1 binding
F:57-107/Domain: RING finger homology <RRN>

Query Match 3.9%; Score 293; DB 2; Length 1560;
Best Local Similarity 23.8%; Pred. No. 1.3e-07;
Matches 151; Conservative 72; Mismatches 200; Indels 212; Gaps 34;

QY 25 HGARPSA--PSFRPQNLRLHPQOPVQYQYEPSPA-----PSTTFNSPAPNPLP 73
Db 296 NAARPGGRPGWEHSN-KLGYLVSPQPIRRGERSCVSRINRGHHSRSQRTQGPS-LP 353
QY 74 PRPDFVFPMPDPSAQGLPPCPPIRPDPNQHMRHPFPVPCFPMPPMPCPNPPVP 133
Db 354 ATPVFVFPVPP-----PLYPPPP-----HTLPLP-----PGVLPPQSPQPP--P 391
QY 134 GAPPGGTPFPWMPPPMPHPP-----PPVMPQOVNV----- 166
Db 392 GQPPTAG---YSVPPGFPAPANISTACFSPCVTAHNTMTTQAPLLSREFFREQK 448
QY 167 -----QYP---PGYSHNFPPPSFNPSFQNNPSSFLPSANNSSPHRLPLPPPLPKAPS 217
Db 449 RLKESKFPYSGSSYSSTDSKSRSGTSRSYSRFSRSHRSYSRSPYP----- 502
QY 218 ERSPERLKHYYDHRDHRSHGGERHRSLSDRRCRSGSDRRQRDSYSDYD-RGRTPS 276
Db 503 -RRRGKSRNY---RSRSRSHG---YHRS-----RSRSPYRRYHRSRSPQAFRCQSPT 550
QY 277 RHRSYRSRERER-HRHR-----DNRSPSLERSYKKEYKR 313
Db 551 K-RNVPRG-ETERYFNRYREVPPVDIKAYGRSVDPRDPFKEKYREWERKYREWEK 608
QY 314 SGRSYGLSVVPEPAGCTPELPGSIIKNNTDSWAP-----PLEIVNHRSPSREKKEARWEEK 369
Db 609 YYKGYAVAGQAPRSA-----NREDFPERLLPLNIRN--SPFTGREEDYAAQG 655
QY 370 DRWSDN-----QSSGDKNYSIKEKEPETMPD-----KNE---EE 403
Db 656 SHRNRLGGNYPEKLSSTDSHNAKNPKSKESENVPGDGKGNKHKHKKRENEEKGE 715
QY 404 EELLKPVMI-----RCHTSEN-----YSSDPMQDQGDSTVVGTSR 440
Db 716 SESFLNPELGLKPRKCRSGSGIDETKDTLTVFPSPREDATPVVDEPMD--AESITPKSVS 773
QY 441 LRDLYDKFEBELGSRQEKAKA-----ARPPWPEPKTKLDELSSESE---CRS 487
Db 774 DKDKREKDKPKVSKDKTKRSDGSAKADKNVLKPSKGPKQKVDGDRKSPREPLKKA 833
QY 488 DEBST-----CSSSSDSEVFDVTAIIRKKAH 514
Db 834 KEBATKIDSVKPSSSSQKDEKVTGT-----PRKAH 863

RESULT 8

B82073
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: B82073
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82073
A:Molecule type: DNA
A>Status: preliminary
A:Residues: 1-235 <HEI>
A:Cross-references: UNIPROT:Q9KPB2; UNIPARC:UPI0000134369; GB:AE004316; GB:AE003852; NID:
A:Experimental source: serogroup O1; strain Ni6961; biotype El Tor
C:Genetics:
A:Gene: VC2461
A:Map position: 1
C:Superfamily: ribonuclease III; double-stranded RNA-binding repeat homology

Query Match 3.8%; Score 285.5; DB 2; Length 225;
Best Local Similarity 32.2%; Pred. No. 2.8e-08;
Matches 75; Conservative 42; Mismatches 101; Indels 15; Gaps 5;

QY 1101 SPVLOKLTFFERAIGVIFTHVLLARAFTLRTVGNHLTLGHNRMEFLGDSIMQLVATE 1160
Db 2 TTPMNKLT---SKLGYTFKTELLNLALTHRSANGK-----HNERLEFLGDSILSFVIAD 53
QY 1161 YLFIHPHHEGHHTLRSLSLVNRTQAKVAELGMOEYAITNDKTRPVGLRKT-K-LAD 1219
Db 54 ELYRRPPKNEGDMGRATLVRGNTLAEGLREFDLGDLKLGPGELKSGGFRDSILAD 113
QY 1220 LLESTIAALYTDKLEYVHTFMNVCFPPRLKBFILNDQNDPKSQIQCCQLTLRTGKBP 1279
Db 114 AVEAIIAIIYDSDLETARSIVLEWYHGLEIKPGASQKDPKTRLOEF-----LQGRRK 168
QY 1280 DPLKYTLQVGPSHARTVTVAVPKG-ERICGGKGPSIQQAEMGAMDALEK 1331
Db 169 PLFVTVTNIKGEAHNQEFVACEVAGMDTPVIGKTSRRKABQAAATALEQ 221

RESULT 9

A83961
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: A83961
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: A83961
A:Molecule type: DNA
A:Residues: 1-263 <STO>
A:Cross-references: UNIPROT:Q9KA05; UNIPARC:UPI0000134340; GB:AP001515; GB:BA000004; NID:
A:Experimental source: strain C-125
C:Genetics:
A:Gene: rncS
C:Superfamily: ribonuclease III; double-stranded RNA-binding repeat homology

Query Match 3.8%; Score 282; DB 2; Length 263;
Best Local Similarity 30.9%; Pred. No. 5.2e-08;
Matches 77; Conservative 50; Mismatches 110; Indels 12; Gaps 5;

QY 1084 HPLQLQEPNTDRLQIETSPVLOKLTFFERAIGVIFTHVLLARAFTLRTVGNH--LTLG 1141
Db 15 HSERRRQP---KRLTLTAKQQQMFDELLTLNLTFAKKLLLVQAFTSSIVNEHRTQSCK 71
QY 1142 HNQRMEFLGDSIMQLVATEYLFTHFPDHHGHHTLRSLSLVNRTQAKVAELGMOEYAI 1201

Db 72 DNERLEFLGDVALEAVSGLYKAFOMSEGDWTKRASIVCEPSLAQAEHLHFGLVL 131
QY 1202 TNDKTRPVG-LRTKTLADLLESFIAALYTDKOLEYVHTFMNVCFPPRLKKEFLNQDWDND 1260
Db 132 LGKGEWMTGGRKPALLADVFSFGALYLDQGDVAFLFLERTIYPKISEGAFSH-WMD 190
QY 1261 PKSQLQCCCLTLRTGKEPDIPLYKTLQTVGPHSHARTYTVAVFKGERICGCGKPSIQQA 1320
Db 191 PKSQLQEF-----IORDNLGHIHYEIOERGPAHNEFVSEVVLNNETTLGVTGGRSKKEA 245
QY 1321 EMGAAMDAL 1329
Db 246 EQHAAQAL 254

RESULT 10
F98012
ribonuclease III (EC 3.1.26.3) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: F98012
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
y, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: F98012
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <KUR>
A:Cross-references: UNIPROT:Q8DPJ8; UNIPARC:UPI00000E35D9; GB:AE007317; PIDN:AAK99930.1;
C:Genetics:
A:Gene: rncS
C:Superfamily: ribonuclease III; double-stranded RNA-binding repeat homology

Query Match 3.8%; Score 281.5; DB 2; Length 232;
Best Local Similarity 32.9%; Pred. No. 4.7e-08;
Matches 79; Conservative 47; Mismatches 91; Indels 23; Gaps 9;
QY 1099 ETSPLVQLKTEPEEAGVIFTHVRLARAFTLRTVGFNH--LTLGHQRMFELGDSIMQL 1156
Db 3 ELQTVLKNHFEI-----FADKKLETAFTHTSYANEHRLKISHNERLEFLGDAVLQL 56
QY 1157 VATEYLFIHPDHEGHLTLRSLLNNRTQAKVAELGMQEVATNDKTRPVGLRTK- 1215
Db 57 LISEYLYKKYKPKPGDLSKLAMIVREESLAGFARDQDF-IKLGKEKSGGRNRD 115
QY 1216 -TLADLESFIAALYTDKOLEYVHTFMNVCFPPRLK--EFILNQDWDNDPKSQLQCCCLTL 1272
Db 116 TLGDFAFEALGALLDKDVAKKEFIQVMIPKVEAGFEFEMITDY---KTHLQE---LL 169
QY 1273 RTEGKEPDIP-LYKTLQTVGPHSHARTYTVAVFKGERICGCGKPSIQQAEMGAMDALEK 1331
Db 170 QVNG---DVAIRYQVISETPAHDKVDFVEVLVEGKSGQGRSKLAEOQAANAWEK 226

RESULT 11
H95144
ribonuclease III [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: H95144
R:Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
non, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: H95144

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <KUR>
A:Cross-references: UNIPROT:Q97QG6; UNIPARC:UPI0000051783; GB:AE005672; PIDN:AAK75353.1;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP1248
C:Superfamily: ribonuclease III; double-stranded RNA-binding repeat homology

Query Match 3.7%; Score 279.5; DB 2; Length 232;
Best Local Similarity 32.5%; Pred. No. 6e-08;
Matches 75; Conservative 48; Mismatches 91; Indels 17; Gaps 8;
QY 1108 TEFEEAIGVIFTHVRLARAFTLRTVGFNH--LTLGHQRMFELGDSIMQLVATEYLFIH 1165
Db 6 TWLKNHFAIEFADKKLETAFTHTSYANEHRLKISHNERLEFLGDAVLQLLSEYLYKK 65
QY 1166 FPDHHEGHLTLRSLLNNRTQAKVAELGMQEVATNDKTRPVGLRTK--TLADLES 1223
Db 66 YPKPBGDLSKLAMIVREESLAGFARDQDF-IKLGKEKSGGRNRDITLGDFAFEA 124
QY 1224 FIAALYTDKLEIVHTFMNVCFPPRLK--EFILNQDWDNDPKSQLQCCCLTLRTGKEPD 1281
Db 125 FLGALLDKDVAKKEFIQVMIPKVEAGFEFEMITDY---KTHLQE---LLQVNG---DV 175
QY 1282 PL-YKTLQTVGPHSHARTYTVAVFKGERICGCGKPSIQQAEMGAMDALEK 1331
Db 176 AIRYQVISETPAHDKVDFVEVLVEGKSGQGRSKLAEOQAANAWEK 226

RESULT 12
A57640
retinoblastoma binding protein RBQ-1 - human
C:Species: Homo sapiens (man)
C>Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: A57640
R:Sakai, Y.; Saijo, M.; Coelho, K.; Kishino, T.; Niikawa, N.; Taya, Y.
Genomics 30, 98-101, 1995
A:Title: cDNA sequence and chromosomal localization of a novel human protein, RBQ-1 (RBB1)
A:Reference number: A57640; MUID:96129310; PMID:8595913
A:Accession: A57640
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-948 <SAK>
A:Cross-references: UNIPROT:Q15290; UNIPARC:UPI000006DB4D; GB:X85133; NID:g728590; PIDN:6
C:Genetics:
A:Gene: GDB:RBBP6
A:Cross-references: GDB:626076
A:Map position: 16p12-16p11.2
C:Keywords: tandem repeat; zinc
F:79-129/Domain: RING finger homology <RNG>

Query Match 3.7%; Score 276; DB 2; Length 948;
Best Local Similarity 23.0%; Pred. No. 5.5e-07;
Matches 149; Conservative 61; Mismatches 208; Indels 230; Gaps 31;
QY 27 ARPSA--PSFRPQNKLHLHPQPPVQYQYEPSSA-----PSTTFNSNPAFNLPPR 75
Db 320 ARPGGGRPCWEHSN-KLGYLVGPPQIRRGERSCYRSINRGHRSRSQRTQGPS-LPAT 377
QY 76 PPFVPPPPMPPSAOGLPCCPIRPPFPNHNQMRHPPFPVPPPCFPMPMPMPMPMPVPGA 135
Db 378 PFFVFPVPPP-----PLYPPPP-----HTLPLP---PGVPPPPQFSPQFP--PGQ 415
QY 136 PRGQGTFFPMMPMPPSPHPPPPVMPVPPQVY-----YQYPP----- 170
Db 416 PPPAG---YSVPPPPGPP-PAPANLSTPWWVSSGVQTAHSNTIPTQAPPISREFFYRQR 471
QY 171 -----GYSHNPPPPPSFNS 184
Db 472 LKEEEKKKSLDEFTNDFAKELMEYKKIQKERRRSFRSKSPYSGSSYSRSTYSKRS 531
QY 185 FQNPSSFLPSANSSSPHFRHLPPYPLKAPSRERSPERLKHDDHRHDHSHGRGERH 244

Db	532	GSTRSRSYSRFSRSHRSYSRSPYP-----RRGRGKSRNY-----RKSRSHG---YH	578
QY	245	RLSDRRGRGSPDRRQDRYSRDYD-RGRTPSRHSYRSRER-----	289
Db	579	RS-----RSRSPRYRHSRSRSPQAFRGQSPNKRNVPOGTEREFYRNYREVPPYDMK	633
QY	290	-----ERRHRDNRRSPSLERSYKKEYKRSYGLSVVVPBPAGCTPELPGE	336
Db	634	AYGRSVDFRDPPEKERYE-----WEKYRWYKYYKYGAAGQPRSA-----	679
QY	337	IIKNTDSWAP-----PLEIVNHRSPSRKRAWEEBKDRMSDNQSSG-----KD	381
Db	680	---NRENFSERPLPLNIRN--SPFTRGRREDVVGQSHRSRNIGSYPEKLSARDGHNQ	734
QY	382	KNTYSIKEKEPEETMPD-----KNBEEBELKPVWIRCTHSENYSSDPM--	427
Db	735	KONTKSEKESENAPGDGKNKHKKRKGEGEGLNPELLETSRK-----SREPTGV	790
QY	428	-DQVGDSVVGTGR-----LRDLYDKFEE---LGSRQEKAKAARPPWPPKTKLDEdle	478
Db	791	EENKTDSLFLPSRDDATPVRD--EPWDAESITFKSVSEKRRER---DKPKAKGDKTKR	845
QY	479	SSSESECEDEDESCSSSSDSE-----VFDVIAEIKRKAHPDRL	518
Db	846	KNDGSAVSKKENIVKPAKGQEKVGDGVRDLDLNLQLKPKERLRL	893
RESULT 13			
T06291			
extensin homolog T9E8.80 - Arabidopsis thaliana			
C:Species: Arabidopsis thaliana (mouse-ear cress)			
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004			
C:Accession: T06291			
R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuel			
submitted to the Protein Sequence Database, April 1999			
A:Reference number: Z15588			
A:Accession: T06291			
A:Molecule type: DNA			
A:Residues: 1-760 <BEV>			
A:Cross-references: UNIPROT:Q9TOK5; UNIPARC:UPI000009FB81; EMBL:AL049608			
A:Experimental source: cultivar Columbia; BAC clone T9E8			
C:Genetics:			
A:Map position: 4			
A:Note: T9E8.80			
Query Match 3.7%; Score 275; DB 2; Length 760;			
Best Local Similarity 35.1%; Pred. No. 4.7e-07;			
Matches 88; Conservative 15; Mismatches 96; Indels 52; Gaps 12;			
QY	14	PGRCPRGRGGHGARSFRQNL-----RLHPQQPPVQYVEPPSAPS-----	60
Db	361	PGRPAQRSPGQCKAFLSRP---PVNCGSFSCGRSVSP-RPPVVTPLPPLSLPSPPPAPPI	416
QY	61	----TTFSNSPAPNFPPEPDE-VPPPPMPPSAQGLPPLPCPIRPPFNHGMHRPPVPVP	115
Db	417	FSTPPTLTSPDPS--PPPPVYSGPPPPPPPPVYSGPPPPPPPPVYSGPPPPPPPP	474
QY	116	CFPPM---PPMPCPNPPVPFGAPPQGTFPFMMPPSPHPPPPPV-----MPQ	162
Db	475	PPPVYVSPPPSPPPPPVYSGPP--PPPPPPVYVSPPPPPVYSGPPPPPPSPAPT	530
QY	163	QVNYQVPPGVSHNFPPPSPNSQNNP--SSFLPSANNSSPHF---RHLPVPVL-----	212
Db	531	PVYCTRPPPPHSPPPPPQSPPPPPYVYSSPPPHSPPPHSPPPHSPPPHPPPIYPYLS	590
QY	213	-PKAPERRSP	222
Db	591	PPPPPTPVSSP	601
RESULT 14			
T48946			

hypothetical protein T15B3.60 - Arabidopsis thaliana			
C:Species: Arabidopsis thaliana (mouse-ear cress)			
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004			
C:Accession: T48946			
R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.; I			
submitted to the Protein Sequence Database, April 2000			
A:Reference number: Z25009			
A:Accession: T48946			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-1531 <JOR>			
A:Cross-references: UNIPROT:Q9LXW7; UNIPARC:UPI000009DAF8; EMBL:AL163975; GSPDB:GN00061;			
A:Experimental source: cultivar Columbia; BAC clone T15B3			
C:Genetics:			
A:Gene: ATSP.T15B3.60			
A:Map position: 3			
A:Introns: 45/2; 100/3; 138/3; 183/3; 227/3; 278/3; 322/1; 357/2; 421/3; 475/2; 584/1; 6			
Query Match 3.7%; Score 274.5; DB 2; Length 1531;			
Best Local Similarity 21.3%; Pred. No. 1.2e-06;			
Matches 247; Conservative 142; Mismatches 420; Indels 351; Gaps 58;			
QY	372	WSDNQGSKDKYTSIKEKEPEETMPDKNEBEEBELKPVWIRCTHSENYSSDPMQDVG	431
Db	455	YSQSQKHAKQSNKSKSIMFL--ERGNPKQRDHLHDLMRREVLIQDPEAPNLKSCPPVYKNG	512
QY	432	DST-VVGTSLRDLYDKFEEELGSRQEKAKAARPPWE---PP-KTKLDED-LESSSES	483
Db	513	HGVKEIGSMVIPDSNITVSEEAATQTSND---PFSRNEQLPCKKLRLDNLLQSNNGKE	569
QY	484	ECESDESDTSCSSSDSSEVFDVIAEIKRKAHPDRLHDEL---WYNDPGQMNIDGP-----	534
Db	570	KVASSKSKSSSAAGSK-----KKELHGTCANALSGTW---GENIDGATQAYK	617
QY	535	---LCKCSAK-----ARRTG-IRHSIYPGERAIK---PCRP-----	564
Db	618	DFCCNIGSEVYSSFLLLESTLAEDVGKVEDMLVLRKLVKASVSPCGQIRLSQBELVK	677
QY	565	-----TNNAGRLFYRITVSPPTNFLTDRPTVIEYDDHEYIEFGSMFAHAPLTNI	615
Db	678	AKYFOOFFPNGMFGKLFVSGSKSGTKREFLLQ-----TDTSSLWHPAFMFLLLVETN	730
QY	616	PLCKVIRFNIDYTHIFIEEMMPENFCVGLGELFSLFRD-ILELYDMNLKGLPFDSP	674
Db	731	DLAS--SATIDWS-----AINSCASIVE--FLKKNLLDLRD-----SDGNQ	768
QY	675	CCPRFHMPFRVRFLPDGQKEVLSMHQILLYLLRCSKALVPBEEHIANMLQWELEWQKVA	734
Db	769	C-----NTSSGQEVL-----LDDKMEETNLTHFANASSDKNS	800
QY	735	BECKGMIVTNPCTKPSVRI--DQDREQFPDVIITFPIIVHFGIRPAQLSYAGDPQYOK	792
Db	801	LEELVIAIHTGRISYIVSAVSDSSAMSPFEVD-----ASSGYATYAEYFN	846
QY	793	LWKSY-VKLRHLIANSP--KVQTKDQK---LAQREELQKIRQK--NTMRREVTVELSS	844
Db	847	--KKYGIIVLAH--PNQPLMKLKQSHAHNLLVDVFNEMVVKTEPKAGNVRKRPNI---	898
QY	845	QGFWKTGIRSDVCQHAMLFPVITHIRYHQCLMHLDKLGYTFQDRCLQLQAMTHFS--H	902
Db	899	-----HAHLPEL-----LARID-----VPRAVLKSIYLLFSVMH	928
QY	903	HLNFGMNPDPHARNSLNCGIRPKYCDRKVHHMHMKKGINTLINIMSLGQDDPTPSRI	962
Db	929	RLESMLASQLREEI-DCSIDNFSISSTSI-----LEAVTTL-----TCPES	969
QY	963	NHNERLEFLGDAAVEFLTSVHLXYLFPSPLEEGGLATYRTAIVONQHAML--AKKLE---	1017
Db	970	FSMERLELLQDSVLKVASCHLPFLKYPDKDEGQLSRQSIINSNLHRLTTSRKLQGYI	1029
QY	1018	----LDPFMLYAHG-----PDLC-----RESDLRH-----	1038
Db	1030	RNGAFEPFRWTAPGQPSLFPVPCCKGIDTRVPLDPKPFETENMTIKIGSCDMGHRWVS	1089

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QY 1039 -AMANCEALIGAVYLEGSLERAKQLFGRLLFN---DPDLREVWLNYPHLPIQLQBPNTD 1094
Db 1090 KSVSDCAEALIGAYVYSGGLSASLHMMKWLGDVDFDNLVVEAINRV--SLRCYIPKED 1147
QY 1095 RQLIETSPVLQKLTPEEAATGVFTFHVRLARAFTLRTVGFNHLTLGHN--ORMEFLGD 1151
Db 1148 -----ELIELEKTKQHEFSAKFLKEAIT-----HSSLRESYSYERLEFLGD 1189
QY 1152 SIMQLVATEYLFTHFPDHHGHHTLRLSSLVNNRTQAKVAE-----ELGM 1196
Db 1190 SVLDFLITRLHFNFTYEQTGSGEMTDLRSACVNNENFAQVAVKNNLHQLRCATVLETOI 1249
QY 1197 QEYAIT---NDKTKR--PVGRLTKTLADLLESFIALYTDKLEYVHTFMNVCFPPRLKE 1251
Db 1250 NDYLSFQKPEDTGRSTPSIQGPKALGDVVESITAGALLIDRLDLDOQVMR--VFEPLLS 1307
QY 1252 FILNQDWN-DPKSQLOQCCLTL---RTEGKEPDIPLYKTLQ-----TVGPSHARTYT 1299
Db 1308 LVTPDKQLQPPYRELNELCDSLGFFRVKCSNDGVKAQATIQQLDDVLTGDSGEQT-- 1365
QY 1300 VAVYFGERIGCGKPSIQQAEMGAAMDALEKYNFPQMAHQKRFICRKY----RQBLKEM 1355
Db 1366 -----NKLALGKAASHLLTQL-----EKRNISRKTSIGDNGQSSMDV 1401
QY 1356 RWREHQERE--PDETEDIX 1373
Db 1402 NLACNHSRETLTSETTEIQ 1421

RESULT 15
G86292
Hypothetical protein F7H2.17 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86292
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.B.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G86292
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1006 <STO>
A:Cross-references: UNIPROT:Q9LMQ1; UNIPARC:UPI00000A2407; GB:AE005172; NID:g8927662; PI
C:Genetics:
A:Map position: 1
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Query Match 3.6%; Score 273.5; DB 2; Length 1006;
Best Local Similarity 32.9%; Pred. No. 8e-07;
Matches 99; Conservative 17; Mismatches 98; Indels 87; Gaps 19;

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QY 3 QGNTCHRMSPHPCGCGCRG-----CHGARPSAPSRPQNLHLHPQOP 47
Db 48 QSNRGRSS-----GSSRNRRSCDPLYOYLFDTCHWHFPFTTFS--PENPEL--PFQP 98
QY 48 PVQYQVEPSPASTTFSNAPNLFPPRPDPFV-FPPMPPSAQGLPPLPCPIRPPFPNHQ 106
Db 99 P-----RPPPRP-----PRRPSRLPPLVPSPPPLNHRP--SPCPPL 138
QY 107 MRHPFPVPCFPMPMPMPNPPVPGAPPQGQTFP-----FMMPSPMPHPPPPVPM 160
Db 139 MPSPPLVPS-PPPPPSPLVSPFP-PPSPPPPPPPPPPPVIVFPPLVPSPPPLPG 196
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Db 197 GDQTT-QPPPLW---LPPPPFGD-ETPPPVFSLPPPLDDEPPP-----MPPITWLPPPDVPA 246
QY 218 ERSPERLKH-----YDDHRHRDHSHGGERHRLDRRGRSPDRRRQDS 263
Db 247 QTSABAFDQIPPLVTTITEAIENPHNSHRHD-----ENKKGIDRRNR-RVKSRRRSRS 299
QY 264 R 264
Db 300 R 300
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Search completed: December 24, 2005, 00:54:08
Job time : 33 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 26, 2005, 11:30:58 ; Search time 2599 Seconds

(without alignments)
12216.466 Million cell updates/sec

Title: US-10-774-974-1

Perfect score: 4764

Sequence: 1 cgtctgtactctgcggtgta.....aaaaaaaaaaaaaaaaaaaaa 4764

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
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9: Geneseq2003bs.*
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12: Geneseq2004as.*
13: Geneseq2004bs.*
14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	4764	100.0	4764	12	ADQ96674
3	4764	100.0	4764	14	AEb47410
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6	4760.8	99.9	4764	13	ADr68726
7	4760.8	99.9	4764	14	ADX03768
8	4760.8	99.9	4764	14	ADY17385
9	4732.4	99.3	5425	12	ADQ22183
10	3376.2	70.9	3603	14	AEa19628
11	2582	54.2	2598	4	AaH13924
12	1735.6	36.4	1784	14	AEa20644
13	1619.6	34.0	1626	9	ACf25385
14	1439.8	30.2	1455	4	AaS33094
15	1398.6	29.4	1458	4	AaS34779
16	1398.6	29.4	1458	10	ADc45937
17	1262.4	26.5	1314	4	AaS33296
18	1262.4	26.5	1314	4	AaS34943
19	1262.4	26.5	1314	10	ADc46101

20	818.8	17.2	897	4	AaH04336	AaH04336 Human cdn
21	770.2	16.2	4275	4	ABL03445	ABL03445 Drosophil
22	725.4	15.2	1003	4	AaF22509	AaF22509 Human bre
23	724	15.2	803	4	AaF22579	AaF22579 Human bre
c						
24	703.8	14.8	6397	4	ABL03444	ABL03444 Drosophil
25	683.4	14.3	833	4	AaF22581	AaF22581 Human bre
26	602.4	12.6	763	4	AaF22510	AaF22510 Human bre
c						
27	581.6	12.2	701	4	AaF22580	AaF22580 Human bre
28	579.8	12.2	591	14	ACL59694	ACL59694 Human col
29	569.6	12.0	744	10	ADD34804	ADD34804 Mouse mit
30	518.2	10.9	578	2	AaZ17689	AaZ17689 Human gen
31	469.4	9.9	633	5	ABV26800	ABV26800 Human pro
32	469.4	9.9	633	5	ABV20994	ABV20994 Human pro
33	469.4	9.9	633	5	ABV20950	ABV20950 Human pro
34	469.4	9.9	633	5	ABV26840	ABV26840 Human pro
c						
35	458.2	9.6	501	4	AaH09845	AaH09845 Human cdn
36	442.4	9.3	5828	5	ABa19864	ABa19864 Human ner
37	442.4	9.3	32223	5	ABa17368	ABa17368 Human ner
38	442.4	9.3	32223	5	ABa19863	ABa19863 Human ner
39	413.4	8.7	9928	5	ABa19865	ABa19865 Human ner
40	411.4	8.6	488	9	ACH33094	ACH33094 Human end
41	405.4	8.5	583	5	ADL45324	ADL45324 Human ova
42	399.2	8.4	3809	6	ABL53489	ABL53489 Human non
43	392.2	8.2	405	4	AaS37351	AaS37351 Novel hum
44	384	8.1	397	3	AaH30538	AaH30538 Human col
45	381.8	8.0	394	5	AaF66326	AaF66326 Novel hum

ALIGNMENTS

RESULT 1
ACD27526
ID ACD27526 standard; cdna; 4764 BP.
XX
AC ACD27526;
XX
DT 18-SEP-2003 (first entry)
XX
DE Human cdna encoding RNase III.
XX
KW Human; ss; gene; RNase III; double stranded RNase; RNA target;
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 246..4370
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FT /transl_except= (pos:297..299,aa:Cys)
FT /transl_except= (pos:3876..3878,aa:Gly)
FT /transl_except= (pos:4278..4280,aa:Gly)
XX
US2003044941-A1.
PN
XX
PD 06-MAR-2003.
XX
PF 20-FEB-2002; 2002US-00079185.
XX
PR 06-JUN-1996; 96US-00659440.
PR 06-JUN-1997; 97US-00870608.
PR 07-JAN-2000; 2000US-00479783.
PR 06-JUL-2001; 2001US-00900425.
XX
PA (CROO/) CROOKE S T.
XX
PI Crooke ST;
XX
DR WPI: 2003-521756/49.
DR P-PSDB; ABU63361.
XX
PT Eliciting a modification of a selected RNA target in a cell, useful for

promoting inhibition of gene expression in a cell, comprises contacting an RNA-like polynucleotide-RNA target duplex with a polypeptide having an RNase III domain.

Example 2: page 13-15: 33pp: English.

The invention relates to eliciting a modification of a selected RNA target in a cell comprises contacting an RNA-like polynucleotide-RNA target duplex with a polypeptide comprising an RNase III domain. Also included are promoting gene silencing in a cell, inhibiting the expression of a gene in a cell comprising employing the method of cited above, promoting inhibition of expression of a gene, a hybrid RNase III (comprising at least one domain from a human RNase III and at least one domain from an RNase III of an organism other than human) and a cell having enhanced RNase III activity over an activity exhibited by a second cell (where the second cell is not enriched with respect to the amount or activity of RNase III polypeptide). The method is useful for eliciting a modification of a selected RNA target in a cell, and for promoting inhibition of expression of a gene in a cell. Compositions comprising RNase III polypeptides or polynucleotides are useful for research, biological and clinical purposes. The polynucleotides may be used in defining the roles of RNase III and the interaction of human RNase III and cellular RNA. Host cells can be used for the production of human RNase III and for identifying agents, which increase or decrease levels of expression or activity of human RNase III in the cell. The present invention encodes human RNase III (a double stranded RNase).

Db ||||| 1681 GTTCCAGTGAATCCGAGTGTGAGTCTGATGAGGACAGCACTGTTCTAGACGCTCAGACT 1740
Qy ||||| 1741 CTGAAAGTTTTGACGTTATGTCAGAAATCAAAACGCAAAAAGGCCACCTGACCGACTTC 1800
Db ||||| 1741 CTGAAAGTTTTGACGTTATGTCAGAAATCAAAACGCAAAAAGGCCACCTGACCGACTTC 1800
Qy ||||| 1801 ATGATGAATCTTGGTACACGATCCAGGCCAGATGAATGATGACCACTCTGCAATGCA 1860
Db ||||| 1801 ATGATGAATCTTGGTACACGATCCAGGCCAGATGAATGATGACCACTCTGCAATGCA 1860
Qy ||||| 1861 GGGCAAAAGCAAGACGACAGCAAGAAATGAGCAGCACTTTATCTGAGAGAGGCCATCA 1920
Db ||||| 1861 GGGCAAAAGCAAGACGACAGCAAGAAATGAGCAGCACTTTATCTGAGAGAGGCCATCA 1920
Qy ||||| 1921 AGCCCTGTGCTCTATGACCAACAATGCTGGCAGACTTTTCCACTACCGGATCA 1980
Db ||||| 1921 AGCCCTGTGCTCTATGACCAACAATGCTGGCAGACTTTTCCACTACCGGATCA 1980
Qy ||||| 1981 CCCGCCCTACGAACTTTTAACTGACAGCGCAACTGTTATAGAAATACGATGATCAGAGT 2040
Db ||||| 1981 CCCGCCCTACGAACTTTTAACTGACAGCGCAACTGTTATAGAAATACGATGATCAGAGT 2040
Qy ||||| 2041 ATATCTTTGAAGATTTCTATGTTTGCACATGCGCCCTGACCAATATTCACATGTTGA 2100
Db ||||| 2041 ATATCTTTGAAGATTTCTATGTTTGCACATGCGCCCTGACCAATATTCACATGTTGA 2100
Qy ||||| 2101 AAGTAATAGATTTCAACATAGACTACACGATTCATTTCAATGAAGAGATGATGCGGAGA 2160
Db ||||| 2101 AAGTAATAGATTTCAACATAGACTACACGATTCATTTCAATGAAGAGATGATGCGGAGA 2160
Qy ||||| 2161 ATTTTGTGTGAAGGGCTTGAACCTTTTCACTGTTCTTATTCAGAGATATTTTGGAAAT 2220
Db ||||| 2161 ATTTTGTGTGAAGGGCTTGAACCTTTTCACTGTTCTTATTCAGAGATATTTTGGAAAT 2220
Qy ||||| 2221 TATATGACTGGAATCTTAAAGTGCCTTTGTTGAAGACAGCCCTCCCTGCTGCCAAGAT 2280
Db ||||| 2221 TATATGACTGGAATCTTAAAGTGCCTTTGTTGAAGACAGCCCTCCCTGCTGCCAAGAT 2280
Qy ||||| 2281 TTCAATTTCAATGCGCAAGTTTGTAAAGTATTTCTTCCAGATGAGGAAAGGAGTGTCTCA 2340
Db ||||| 2281 TTCAATTTCAATGCGCAAGTTTGTAAAGTATTTCTTCCAGATGAGGAAAGGAGTGTCTCA 2340
Qy ||||| 2341 TGCACAGATTTCTCTGTACTTGTAAAGTGTGAGCAAAAGCCCTGCTGAGGAGGAGA 2400
Db ||||| 2341 TGCACAGATTTCTCTGTACTTGTAAAGTGTGAGCAAAAGCCCTGCTGAGGAGGAGA 2400
Qy ||||| 2401 TTGCCAAATATGCTTCAGTGGGAGGAGCTGGAGTGGCAGAAATATGACAGAAATGCAAG 2460
Db ||||| 2401 TTGCCAAATATGCTTCAGTGGGAGGAGCTGGAGTGGCAGAAATATGACAGAAATGCAAG 2460
Qy ||||| 2461 GCATGATTTGTTACCAACCTCGGAGCGAAACCAAGCTCTGCTCGTATCGATCAACTGGATC 2520
Db ||||| 2461 GCATGATTTGTTACCAACCTCGGAGCGAAACCAAGCTCTGCTCGTATCGATCAACTGGATC 2520
Qy ||||| 2521 GTGAACAGTTCAACCCCGATGTAATTAATTTTCCGATATGCTCACTTTGGGATACGCC 2580
Db ||||| 2521 GTGAACAGTTCAACCCCGATGTAATTAATTTTCCGATATGCTCACTTTGGGATACGCC 2580
Qy ||||| 2581 CTGCAAGTTGATTTGACAGAGACCCACAGTACCAAAAATGTTGGAAGATTTATGTA 2640
Db ||||| 2581 CTGCAAGTTGATTTGACAGAGACCCACAGTACCAAAAATGTTGGAAGATTTATGTA 2640
Qy ||||| 2641 AACTTCGCCACCTCTTAGCAAAATAGTCCCAAAAGTCAAACTGACAAACAGAAAGCTGG 2700
Db ||||| 2641 AACTTCGCCACCTCTTAGCAAAATAGTCCCAAAAGTCAAACTGACAAACAGAAAGCTGG 2700
Qy ||||| 2701 CACAGAGGAGGAGCCCTTCAAAAATAACGCGAGAGAAATCAATGAGACGAGAGTAA 2760
Db ||||| 2701 CACAGAGGAGGAGCCCTTCAAAAATAACGCGAGAGAAATCAATGAGACGAGAGTAA 2760
Qy ||||| 2761 CGGTGGAGCTAATAGTACCAAGATTTCTGAAATCTGGCAATCCGTTCTGATGCTGTGAGC 2820

Db ||||| 2761 CGGTGGAGCTAATAGTACCAAGATTTCTGAAATCTGGCAATCCGTTCTGATGCTGTGAGC 2820
Qy ||||| 2821 ATGCAATGATGCTACTGTTCTGACCCATCATATCCGCTACCAATGCGCTTAATGCAAT 2880
Db ||||| 2821 ATGCAATGATGCTACTGTTCTGACCCATCATATCCGCTACCAATGCGCTTAATGCAAT 2880
Qy ||||| 2881 TGGACAAGTTGATAGGATATATTTTCCAAGATGCTTTGTCAGCTGGCCATGACTC 2940
Db ||||| 2881 TGGACAAGTTGATAGGATATATTTTCCAAGATGCTTTGTCAGCTGGCCATGACTC 2940
Qy ||||| 2941 ATCCAAGTCAATTTAAATTTTGGAAATGAAATCTGATCATGCCAGAAATTTCAATTTCTA 3000
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Db ||||| 3001 ACTGTGGAATTCGGCAGCCCAATACGGAGACAGAAAAGTTTCAATGACATGCGGGA 3060
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Db ||||| 3061 AGAAAGGATTAACACCTTTGATAAATATCATGTGACGCTTGGCCAAAGATGACCCAACTC 3120
Qy ||||| 3121 CCTCGAGGATTAACCAATGAACGTTTGGAAATTCCTGGGTGATGCTGTTTGAATTTTC 3180
Db ||||| 3121 CCTCGAGGATTAACCAATGAACGTTTGGAAATTCCTGGGTGATGCTGTTTGAATTTTC 3180
Qy ||||| 3181 TGACAGCGTCAATTTGATGATATTTGTTTCTTAGTCTGGAAGAGAGATTTAGCAACCT 3240
Db ||||| 3181 TGACAGCGTCAATTTGATGATATTTGTTTCTTAGTCTGGAAGAGAGATTTAGCAACCT 3240
Qy ||||| 3241 ATCGGACTGCCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300
Db ||||| 3241 ATCGGACTGCCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300
Qy ||||| 3301 ATCCATTTATGCTGATGCTCAACGCTTGAACCTTTGTAGAGAAATCGGACCTTCGACATG 3360
Db ||||| 3301 ATCCATTTATGCTGATGCTCAACGCTTGAACCTTTGTAGAGAAATCGGACCTTCGACATG 3360
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Qy ||||| 3781 GCTCTTTGGTGAATTAATGAACTCAGGCCAAGGATGAGGAGGAGCTGGGCAATGCAAGAGT 3840
Db ||||| 3781 GCTCTTTGGTGAATTAATGAACTCAGGCCAAGGATGAGGAGGAGCTGGGCAATGCAAGAGT 3840
Qy ||||| 3841 ACGCCATTAACCAACGACCAAGAGCCCTGTCGCTTCCGACCAAGAGCTTGGCGG 3900
Db ||||| 3841 ACGCCATTAACCAACGACCAAGAGCCCTGTCGCTTCCGACCAAGAGCTTGGCGG 3900

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Db |||||
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QY 4141 CTGTGGCTGTTTATTTTCAAGGGAGAAAGATAGGCTGTGGGAAAGGACCAAGTATTTCAGC 4200
Db |||||
QY 4141 CTGTGGCTGTTTATTTTCAAGGGAGAAAGATAGGCTGTGGGAAAGGACCAAGTATTTCAGC 4200
Db |||||
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Db |||||

RESULT 2

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ID ADQ96674 standard; cdna; 4764 BP.
XX
AC ADQ96674;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human ribonuclease III (RNase III) cdna.
XX
KW Human; ribonuclease III; RNase III; research purpose; biological purpose;

clinical purpose; gene; cellular interaction; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 246..4370
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FT /product= "Human ribonuclease III protein"
FT /transl_except= (pos:297..299, aa:Cys)
FT /transl_except= (pos:3876..3878, aa:Gly)
FT /transl_except= (pos:4278..4280, aa:Gly)
XX
PN US2004126867-A1.

PD 01-JUL-2004.

XX 09-FEB-2004; 2004US-00774974.

XX 06-JUL-2001; 2001US-00900425.

XX (CROO/) CROOKE S T.
XX (WUHH/) WU H.

PI Crooke ST, Wu H;

XX WPI: 2004-516913/49.

DR P-PSDB; ADQ96675.

DR GENBANK; AF189011.

XX New isolated nucleic acid molecule encoding human RNase III, useful for

PT research, biological, or clinical purposes, e.g. defining the roles of

PT RNase III and the interaction of human RNase III and cellular RNA.

XX Claim 2; SEQ ID NO 1; 31pp; English.

XX The invention relates to human ribonuclease III (RNase III) and its

CC corresponding nucleic acid sequence. The polynucleotide sequence of the

CC invention is useful for research, biological and clinical purposes. It is

CC useful in defining the roles of RNase III and the interaction of human

CC RNase III and cellular RNA. The present sequence is human RNase III cDNA.

XX Query Match 100.0%; Score 4764; DB 12; Length 4764;

XX Best Local Similarity 100.0%; Pred No. 0;

XX Matches 4764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTGTCTTGTGTACCTGCGGTAGTAGCTGCTTGTCTCTGACGCGCATCTCGGCGCCGAG 60

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Db 61 AGCTTTTATAGTGTGCTTTTCCCGGGATGTGAAGGATACAGAAATGACTGTGAATCAA 120

QY 121 CCCATATCATCAAGGAGCTGATAATCTAGTGAAGAGTTAGACGTGTGCATCTTCACTA 180

Db 121 CCCATATCATCAAGGAGCTGATAATCTAGTGAAGAGTTAGACGTGTGCATCTTCACTA 180

QY 181 TGATATGAGGCGAGTCTCTGAGCTTATATTTCTCTGTGGAAGATGTGATATCCAGCGGA 240

Db 181 TGATATGAGGCGAGTCTCTGAGCTTATATTTCTCTGTGGAAGATGTGATATCCAGCGGA 240

QY 241 ACATCATGATGAGGAGAAACATGTGCAGAGATGTCTCCACCGGACGAGGGCGTC 300

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QY 301 CCGGAGGACGAGGAGACATGAGCCAGACCTTCAGCACCATCTTTTAGGCCCCAAAATC 360

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Qy 481 TACCCCTTCCCCACCAACGCTCCTCAGCGCAAGGCCCTCTTCCGCCCTGCCAATCA 540
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Qy 541 GGCAGCTTTTCCCAACCAACGATGAGGACCCCTTCCAGTTCTCTCTGTTTTCCTC 600
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Qy 601 CCAATGCCACCAATGCTTGTCTTAATAACCCCGCAGTCCCTGGGGCACTCTCTGGAC 660
Db 601 CCAATGCCACCAATGCTTGTCTTAATAACCCCGCAGTCCCTGGGGCACTCTCTGGAC 660
Qy 661 AAGGCACTTTCCCTTTCATGATGCCCTCCCTCCATGCTCATCCCGCCGCCCTCCAG 720
Db 661 AAGGCACTTTCCCTTTCATGATGCCCTCCCTCCATGCTCATCCCGCCGCCCTCCAG 720
Qy 721 TCATGCGCAGCAGGTTAATTATCAGTACCTCCGGGCTATTCTCACCAACCTTCCAC 780
Db 721 TCATGCGCAGCAGGTTAATTATCAGTACCTCCGGGCTATTCTCACCAACCTTCCAC 780
Qy 781 CTCGCCAGTTTAAATAGTTTCCAGAAACACCCCTAGTTTCTTCTGCCCCAGTGTAAATA 840
Db 781 CTCGCCAGTTTAAATAGTTTCCAGAAACACCCCTAGTTTCTTCTGCCCCAGTGTAAATA 840
Qy 841 GCAGTAGTCTCATTTTTCAGACATCTCCCTCCATACCACCTCCCAAGGCTCCAGTGAGA 900
Db 841 GCAGTAGTCTCATTTTTCAGACATCTCCCTCCATACCACCTCCCAAGGCTCCAGTGAGA 900
Qy 901 GAAAGTCCCAGAAAGGCTGAAACACTATGATGACCAAGGACCCAGACCAACAGTCATG 960
Db 901 GAAAGTCCCAGAAAGGCTGAAACACTATGATGACCAAGGACCCAGACCAACAGTCATG 960
Qy 961 GCGAGGTGAGAGGATCGGTCCCTGGATCGCGGAGGAGCGCAGTCCGACAGGA 1020
Db 961 GCGAGGTGAGAGGATCGGTCCCTGGATCGCGGAGGAGCGCAGTCCGACAGGA 1020
Qy 1021 GAAGACAAGACGCGGTACAGATCTGATATGACCGAGGAGAACACCATCTCGCCACC 1080
Db 1021 GAAGACAAGACGCGGTACAGATCTGATATGACCGAGGAGAACACCATCTCGCCACC 1080
Qy 1081 GCAGCTACCAACGAGCAGAGCGAGAACCGGAGAGACACAGGCAATCGAGCAACCGAA 1140
Db 1081 GCAGCTACCAACGAGCAGAGCGAGAACCGGAGAGACACAGGCAATCGAGCAACCGAA 1140
Qy 1141 GATCACCATCTCTGGAAGGTCCTACAAAAAGAGTATAAGAGATCTGGAAGAGTTACG 1200
Db 1141 GATCACCATCTCTGGAAGGTCCTACAAAAAGAGTATAAGAGATCTGGAAGAGTTACG 1200
Qy 1201 GTTTATCGGTGTTCTGAACTCTGATGATGACACAGAAATACCTGGGGAGATTATTA 1260
Db 1201 GTTTATCGGTGTTCTGAACTCTGATGATGACACAGAAATACCTGGGGAGATTATTA 1260
Qy 1261 AAAATACAGATTTCTGGGCCCCACCCCTGGAGATCTGAAATCATCCCTCCCAAGTAGG 1320
Db 1261 AAAATACAGATTTCTGGGCCCCACCCCTGGAGATCTGAAATCATCCCTCCCAAGTAGG 1320
Qy 1321 AGAAGAGAGAGCTCTGTTGGGAGGAGAAAAAGACCGTTGGAGTGAACAACAGAGTTCTG 1380
Db 1321 AGAAGAGAGAGCTCTGTTGGGAGGAGAAAAAGACCGTTGGAGTGAACAACAGAGTTCTG 1380
Qy 1381 GCAAGACAAGAACTATACCTCAATCAAGGAAAAAGAGCCCGAGGAGACCATGCTTGACA 1440
Db 1381 GCAAGACAAGAACTATACCTCAATCAAGGAAAAAGAGCCCGAGGAGACCATGCTTGACA 1440
Qy 1441 AGAATGAGGAGGAGAGAGACTTCTTAAGCCTGTGTGATTCGATGCACTCATTTAG 1500
Db 1441 AGAATGAGGAGGAGAGAGACTTCTTAAGCCTGTGTGATTCGATGCACTCATTTAG 1500

Qy 1501 AAAAATACTACTCCAGTGAACCCATGGATCAGGTGGGAGATTCTACAGTGGTTGGAACGA 1560
Db 1501 AAAAATACTACTCCAGTGAACCCATGGATCAGGTGGGAGATTCTACAGTGGTTGGAACGA 1560
Qy 1561 GTAGGCTTCTGACTTATATGACAAATTTAGGAGGAGTTGGGAGCAGCAAGAAAAGG 1620
Db 1561 GTAGGCTTCTGACTTATATGACAAATTTAGGAGGAGTTGGGAGCAGCAAGAAAAGG 1620
Qy 1621 CCAAGCTCTCTCGGCTCCGTGGGAACCTCCAAAGAAGCTCGATGAAGATTATAGAGA 1680
Db 1621 CCAAGCTCTCTCGGCTCCGTGGGAACCTCCAAAGAAGCTCGATGAAGATTATAGAGA 1680
Qy 1681 GTTCCAGTGAATCCGAGTGTGAGTCTGATGAGGACAGCACTTCTTAGCAGTCAAGACT 1740
Db 1681 GTTCCAGTGAATCCGAGTGTGAGTCTGATGAGGACAGCACTTCTTAGCAGTCAAGACT 1740
Qy 1741 CTGAAGTTTTTTCAGCTTTATTCAGAAATCAAAACGCAAAAAGGCCACCTGACCGACTTC 1800
Db 1741 CTGAAGTTTTTTCAGCTTTATTCAGAAATCAAAACGCAAAAAGGCCACCTGACCGACTTC 1800
Qy 1801 ATGATGAACCTTTGGTACAACAGATCCAGGCCAGATGAATGATGACCACTCTGCAATGCA 1860
Db 1801 ATGATGAACCTTTGGTACAACAGATCCAGGCCAGATGAATGATGACCACTCTGCAATGCA 1860
Qy 1861 GGCAGAGGCAAGACGACAGGAATTTAGGCAAGCAATTTATCTGAGAGAGGCCCATCA 1920
Db 1861 GGCAGAGGCAAGACGACAGGAATTTAGGCAAGCAATTTATCTGAGAGAGGCCCATCA 1920
Qy 1921 AGCCCTGCTGCTCTATGACCAACATGCTGGCAGACTTTTCCACTACCCGATCACAAGTCT 1980
Db 1921 AGCCCTGCTGCTCTATGACCAACATGCTGGCAGACTTTTCCACTACCCGATCACAAGTCT 1980
Qy 1981 CCCCGCTACGAACTTTTAACTGACAGGCCAACTGTTATAGAATACGATGATCAGAGT 2040
Db 1981 CCCCGCTACGAACTTTTAACTGACAGGCCAACTGTTATAGAATACGATGATCAGAGT 2040
Qy 2041 ATATCTTTGAGAGATTTTCTATGTTTGCATGCCCCCTGACCAATATTTCCACTGTGTA 2100
Db 2041 ATATCTTTGAGAGATTTTCTATGTTTGCATGCCCCCTGACCAATATTTCCACTGTGTA 2100
Qy 2101 AAGTAATAGATTCAACATAGACTACAGATTCATTTCAITGAAAGATGATGCCGGAGA 2160
Db 2101 AAGTAATAGATTCAACATAGACTACAGATTCATTTCAITGAAAGATGATGCCGGAGA 2160
Qy 2161 ATTTTGTGTGAAAGGCTTGAACCTTTTCACTGTTCTTATTCAGAGATATTTTGGAAAT 2220
Db 2161 ATTTTGTGTGAAAGGCTTGAACCTTTTCACTGTTCTTATTCAGAGATATTTTGGAAAT 2220
Qy 2221 TATATGACTGGAATCTTAAAGGTCCTTTGTTTGAAGACAGACCCCTCCTGCTGCCAAGAT 2280
Db 2221 TATATGACTGGAATCTTAAAGGTCCTTTGTTTGAAGACAGACCCCTCCTGCTGCCAAGAT 2280
Qy 2281 TTTCAATTCATGCGCTTTTGAAGATTTCTTCCAGATGCGGAGGAGGAGTCTCTCCA 2340
Db 2281 TTTCAATTCATGCGCTTTTGAAGATTTCTTCCAGATGCGGAGGAGGAGTCTCTCCA 2340
Qy 2341 TGCACACAGATTTCTCTGACTTTGTTAAGGTGAGCAAAAGCCCTGGTGTCTGAGGAGAGA 2400
Db 2341 TGCACACAGATTTCTCTGACTTTGTTAAGGTGAGCAAAAGCCCTGGTGTCTGAGGAGAGA 2400
Qy 2401 TTGCCAAATATGCTTCAAGTGGGAGGAGTGGAGTGGCAGAAAATATGAGAGAAATGCAAG 2460
Db 2401 TTGCCAAATATGCTTCAAGTGGGAGGAGTGGAGTGGCAGAAAATATGAGAGAAATGCAAG 2460
Qy 2461 GCATGATGTTTACCAACCTCGGAGCAACCAAGCTCTGTCGATCAACTGGAATC 2520
Db 2461 GCATGATGTTTACCAACCTCGGAGCAACCAAGCTCTGTCGATCAACTGGAATC 2520
Qy 2521 GTGAACAGTTCAACCCCGATGTATTCTTTTCCGATATCGTCCACTTTGGGATACGCC 2580
Db 2521 GTGAACAGTTCAACCCCGATGTATTCTTTTCCGATATCGTCCACTTTGGGATACGCC 2580

Db	4741	TA	AAAAAAAAAAAAAAAAAAAAA	4764	
		RESULT 3			
		AEBA47410			
ID		AEBA47410	standard; cDNA; 4764 BP.		
XX		AC			
XX		AC			
XX		DT	22-SEP-2005 (first entry)		
XX		DE	Human ribonuclease III (RNase III) cDNA, SEQ ID NO: 1.		
XX		KW	Ribonuclease; gene silencing; gene; ss.		
XX		OS	Homo sapiens.		
XX		PH	Key	Location/Qualifiers	
FT		CDS	246..4370		
FT			/*tag= a		
FT			/product= "Human ribonuclease III (RNase III) protein"		
FT			/transl_except= (pos:297..299, aa:Cys)		
FT			/transl_except= (pos:3876..3879, aa:Gly)		
FT			/transl_except= (pos:4278..4280, aa:Gly)		
XX					
PN			US2005159384-A1.		
XX					
XX			21-JUL-2005.		
XX			02-DEC-2004; 2004US-00001993.		
XX			06-JUL-2001; 2001US-00900425.		
XX			20-FEB-2002; 2002US-00079185.		
XX			(ISIS-) ISIS PHARM INC.		
PA					
XX					
PI			Crooke ST;		
XX					
XX			WPI; 2005-512270/52.		
DR			P-PSDB; AEB47411.		
DR			GENBANK; AF189011.		
XX					
PT			Use of RNase III for eliciting modification of a selected RNA target,		
PT			promoting gene silencing of a gene, inhibiting the expression of a gene,		
PT			promoting inhibition of expression of a gene, or eliciting modification		
PT			of an RNA target.		
XX					
PS			Example 2; SEQ ID NO 1; 32pp; English.		
XX					
CC			The present invention relates to ribonuclease III (RNase III) nucleic		
CC			acids and their encoding proteins. RNase III is an endoribonuclease that		
CC			cleaves double stranded RNA. The invention is useful for eliciting		
CC			modification of a selected RNA target in a cell, promoting gene silencing		
CC			of a gene, inhibiting the expression of a gene, promoting inhibition of		
CC			expression of a gene and eliciting modification of a RNA target in a		
CC			cell. The present sequence is human ribonuclease III (RNase III) cDNA.		
XX					
SQ			Sequence 4764 BP; 1379 A; 1140 C; 1082 G; 1163 T; 0 U; 0 Other;		
			Query Match	100.0%;	Score 4764; DB 14; Length 4764;
			Best Local Similarity	100.0%;	Pred. NO. 0;
			Matches 4764; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
Qy	1	CTGCTGTGTACTCGGCTAGCTAGCTGCTTTGCTCTGACGGCGATCTCGGGCCCGAG	60		
Db	1	CTGCTGTGTACTCGGCTAGCTAGCTGCTTTGCTCTGACGGCGATCTCGGGCCCGAG	60		
Qy	61	AGCCTTTATAGTGTGCTTTTCCGGGGATGGAAGGATACAGAATGACTGTGAATCAA	120		
Db	61	AGCCTTTATAGTGTGCTTTTCCGGGGATGGAAGGATACAGAATGACTGTGAATCAA	120		
Qy	121	CCCATATCATCAGGAGCTGATAATCTAGTGGAAAGAGTTAGCGTGTGCATCTTCACTA	180		

	Query Match	100.0%	Score 4764;	DB 14;	Length 4764;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 4764;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CTGCTCTGGTACCTGGCGGTAGCTAGCTGGCTTTGCTCTGACGGCGATCTCGGGGCCGAG	60		
Db	1	CTGCTCTGGTACCTGGCGGTAGCTAGCTGGCTTTGCTCTGACGGCGATCTCGGGGCCGAG	60		
Qy	61	AGCCTTTTATAGGTGTCTTTTCCCGGGGATGTGAAGGATACAGAAATGACTGTGAATCAA	120		
Db	61	AGCCTTTTATAGGTGTCTTTTCCCGGGGATGTGAAGGATACAGAAATGACTGTGAATCAA	120		
Qy	121	CCCATATCATCAAGAGCTGTATATCTAGTGGAAAGATTAGCGTGTGCATPACTTCACTA	180		

QY	1261	AAAAACAGATCTTTGGGCCCCCACCCTCGAGATTGTGAATCATCGCTCCCACAGTAGGG	1320	2341	TGCACAGATTCCTCTGTACTTTGAAGTGCAGCAAAAGCCCTGTGCTGAGGAGGA	2400
DB	1261	AAAAACAGATCTTTGGGCCCCCACCCTCGAGATTGTGAATCATCGCTCCCACAGTAGGG	1320	2341	TGCACAGATTCCTCTGTACTTTGAAGTGCAGCAAAAGCCCTGTGCTGAGGAGGA	2400
QY	1321	AGAAAGAGAGAGCTCGTTGGGAGGAGAAAAAGACCGTTGGAGTGACAAACAGAGTTCTG	1380	2401	TTGCCAATATGCTTCAGTGGGAGGAGCTGGAGTGCAGAAATATGCAGAGAAATGCAAAAG	2460
DB	1321	AGAAAGAGAGAGCTCGTTGGGAGGAGAAAAAGACCGTTGGAGTGACAAACAGAGTTCTG	1380	2401	TTGCCAATATGCTTCAGTGGGAGGAGCTGGAGTGCAGAAATATGCAGAGAAATGCAAAAG	2460
QY	1381	GCAAGACAAGAACTATACCTCAATCAAGGAAAAAGAGCCGAGGAGACCATGCTGTGACA	1440	2461	GCATGATTTGTACCAACCTCGGACGAAACCAAGCTCTGTCCGTATCGATCAACTGGATC	2520
DB	1381	GCAAGACAAGAACTATACCTCAATCAAGGAAAAAGAGCCGAGGAGACCATGCTGTGACA	1440	2461	GCATGATTTGTACCAACCTCGGACGAAACCAAGCTCTGTCCGTATCGATCAACTGGATC	2520
QY	1441	AGAAAGAGAGAGAGAGAGACTTCTTAAGCCTGTGTGGATTCCGATGCATCTATTTCAG	1500	2521	GTGAACAGTTCAACCCCGATGTGATTACTTTTCCGATATCGTCCACTTTGGGATACGCC	2580
DB	1441	AGAAAGAGAGAGAGAGAGAGACTTCTTAAGCCTGTGTGGATTCCGATGCATCTATTTCAG	1500	2521	GTGAACAGTTCAACCCCGATGTGATTACTTTTCCGATATCGTCCACTTTGGGATACGCC	2580
QY	1501	AAAACTACTACTCCAGTGACCCCATGGATCAGGTGGGAGATTCTACAGTGGTTGAAACGA	1560	2581	CTGCAAGTTGAGTTATGCAAGAGACCCACAGTACCAAACTGTGGAAAGAGTTATGTGA	2640
DB	1501	AAAACTACTACTCCAGTGACCCCATGGATCAGGTGGGAGATTCTACAGTGGTTGAAACGA	1560	2581	CTGCAAGTTGAGTTATGCAAGAGACCCACAGTACCAAACTGTGGAAAGAGTTATGTGA	2640
QY	1561	GTAGGCTTCGTGACTTATATGACAAATTTGAGAGGAGTTGGGAGCAGGCAAGAAAAGG	1620	2641	AACTTGGCCACCTCTAGCAATAGTCCCARAAGTCAAAACAACTGCACAAACAGAGCTGG	2700
DB	1561	GTAGGCTTCGTGACTTATATGACAAATTTGAGAGGAGTTGGGAGCAGGCAAGAAAAGG	1620	2641	AACTTGGCCACCTCTAGCAATAGTCCCARAAGTCAAAACAACTGCACAAACAGAGCTGG	2700
QY	1621	CCAAAGCTGCTCGGCCCTCGTGGGACCTCCAAAGCAGAGCTCGATGAAGATTTAGAGA	1680	2701	CACAGAGGAGGAAAGCCCTCCAAAAATAACGCAGAGAATAACAATGAGACGAGAAGTAA	2760
DB	1621	CCAAAGCTGCTCGGCCCTCGTGGGACCTCCAAAGCAGAGCTCGATGAAGATTTAGAGA	1680	2701	CACAGAGGAGGAAAGCCCTCCAAAAATAACGCAGAGAATAACAATGAGACGAGAAGTAA	2760
QY	1681	GTTTCCAGTCAATCCGAGTGTGATGATGAGGACAGCACCTGTTCTAGCAGCTCAGACT	1740	2761	CGGTGGAGCTAAGTAGCCAAAGATTCTGGAAAACTGGGCATCCGTTCTGATGTCTGTGAG	2820
DB	1681	GTTTCCAGTCAATCCGAGTGTGATGATGAGGACAGCACCTGTTCTAGCAGCTCAGACT	1740	2761	CGGTGGAGCTAAGTAGCCAAAGATTCTGGAAAACTGGGCATCCGTTCTGATGTCTGTGAG	2820
QY	1741	CTGAAGTTTTGACGTTATTGACAGAAATCAACGCAAAAAAGGCCACCTGACCGACTTC	1800	2821	ATGCAATGATGCTACTGTTCTGACCCCATCATATCCGTTACCACCAATSCCTAAATGCAAT	2880
DB	1741	CTGAAGTTTTGACGTTATTGACAGAAATCAACGCAAAAAAGGCCACCTGACCGACTTC	1800	2821	ATGCAATGATGCTACTGTTCTGACCCCATCATATCCGTTACCACCAATSCCTAAATGCAAT	2880
QY	1801	ATGATGAATTTGGTACACAGATCCAGGCCAGATGATGATGATGATGATGATGATGATGAT	1860	2881	TGGACAAGTTGATAGGATATATCTTTCCAAAGATCGTTGTCTGTGACGTGGCCATGACTC	2940
DB	1801	ATGATGAATTTGGTACACAGATCCAGGCCAGATGATGATGATGATGATGATGATGATGAT	1860	2881	TGGACAAGTTGATAGGATATATCTTTCCAAAGATCGTTGTCTGTGACGTGGCCATGACTC	2940
QY	1861	GGCAAGGCAAGACGACAGGAAATPAGGACAGACATTTTATCTGTGAGAGAGGCCATCA	1920	2941	ATCCAAGTCATCAATTTAAATTTTGGAAATGAAATCTCTGATCATGCCAGGAATTCATTA	3000
DB	1861	GGCAAGGCAAGACGACAGGAAATPAGGACAGACATTTTATCTGTGAGAGAGGCCATCA	1920	2941	ATCCAAGTCATCAATTTAAATTTTGGAAATGAAATCTCTGATCATGCCAGGAATTCATTA	3000
QY	1921	AGCCCTGTCTGCTATGACCAACATGCTGGCAGACTTTTCCACTACCGGATCAGACTCT	1980	3001	ACTGTGGAATTCGGCAGCCCAATACGGAGACAGAAAAAGTTTATCATCATGCAATCGGA	3060
DB	1921	AGCCCTGTCTGCTATGACCAACATGCTGGCAGACTTTTCCACTACCGGATCAGACTCT	1980	3001	ACTGTGGAATTCGGCAGCCCAATACGGAGACAGAAAAAGTTTATCATCATGCAATCGGA	3060
QY	1981	CCCCGCTACGAACTTTTAACTGACAGGCCAACTGTTATAGAATACGATGATCAGACT	2040	3061	AGAAAGGGAATTAACACCTTTGATAAATATCATGTACGCCCTTGGCCAAAGATGACCCA	3120
DB	1981	CCCCGCTACGAACTTTTAACTGACAGGCCAACTGTTATAGAATACGATGATCAGACT	2040	3061	AGAAAGGGAATTAACACCTTTGATAAATATCATGTACGCCCTTGGCCAAAGATGACCCA	3120
QY	2041	ATATCTTTGAAGGATTTCTATGTTTGCATGCCCCCTCGACCAATATTTCACTGTGTA	2100	3121	CTCGAGGATTAACCAATGAACCGTTTGGAAATTCCTGGGTGATGCTGTTGTTGAATTTTC	3180
DB	2041	ATATCTTTGAAGGATTTCTATGTTTGCATGCCCCCTCGACCAATATTTCACTGTGTA	2100	3121	CTCGAGGATTAACCAATGAACCGTTTGGAAATTCCTGGGTGATGCTGTTGTTGAATTTTC	3180
QY	2101	AAGTAAATAGATTCACATAGACTACACGATTCATTTCAATTGAAGAGATGATGCCGAGA	2160	3181	TGACCAAGCTTCATTTGTACTATTTGTTTCCCTAGTCTGGAAGAAGAGGATTAGCAACCT	3240
DB	2101	AAGTAAATAGATTCACATAGACTACACGATTCATTTCAATTGAAGAGATGATGCCGAGA	2160	3181	TGACCAAGCTTCATTTGTACTATTTGTTTCCCTAGTCTGGAAGAAGAGGATTAGCAACCT	3240
QY	2161	ATTTTGTGTGAAGGCTTGAATCTTTTCACTGTTCCTATTCAGAGATATTTTGAAT	2220	3241	ATCGGACTGCCATTTGTTTCCAGACCTTTGCCATGCTAGCAATGCTAGCAAGAAATTTGA	3300
DB	2161	ATTTTGTGTGAAGGCTTGAATCTTTTCACTGTTCCTATTCAGAGATATTTTGAAT	2220	3241	ATCGGACTGCCATTTGTTTCCAGACCTTTGCCATGCTAGCAATGCTAGCAAGAAATTTGA	3300
QY	2221	TATATCACTGGAATCTTAAAGTCTCTTTTGAAGACAGCCCTCCCTGCTGCCCAAGAT	2280	3301	ATCCATTTATGCTGTATGCTCAACCGGCTTGACCTTTTGTATAGAAATCGGACCTTCGACATG	3360
DB	2221	TATATCACTGGAATCTTAAAGTCTCTTTTGAAGACAGCCCTCCCTGCTGCCCAAGAT	2280	3301	ATCCATTTATGCTGTATGCTCAACCGGCTTGACCTTTTGTATAGAAATCGGACCTTCGACATG	3360
QY	2281	TTCAATTTCAATCGCTTTTGTGAAGATTTCTTCAGATGGAAGAAAGGAGTGTCTCCA	2340	3361	CAATGGCCAAATTTGTTTGAAGGCTTAAATAGGAGCTGTTTACTTTGAGGGAAGCTCGAGG	3420
DB	2281	TTCAATTTCAATCGCTTTTGTGAAGATTTCTTCAGATGGAAGAAAGGAGTGTCTCCA	2340	3361	CAATGGCCAAATTTGTTTGAAGGCTTAAATAGGAGCTGTTTACTTTGAGGGAAGCTCGAGG	3420
				3421	AAGCCAAAGCAGTTATTTTGGACGCTTGTCTCTTTAATGATCCGGACCTGCGCGAAGTCTGGC	3480

Db	3421		AAGCCAAGCAGTATATTTGGACGCTTGCTCTTTAATGATCCGGAGCTCTCGCGAAGTCTGGC	3480
Qy	3481	TCAAATATCTCTCCACCCACTCCAACTCAAGAAGCCAAATACTGATCGACCAACTTAATG	3540	
Db	3481	TCAAATATCTCTCCACCCACTCCAACTCAAGAAGCCAAATACTGATCGACCAACTTAATG	3540	
Qy	3541	AAACTTCTCCAGTTCTCAAAAACTTACTGAGTTTGAAGAGCAATTTGGAGTAATTTTTTA	3600	
Db	3541	AAACTTCTCCAGTTCTCAAAAACTTACTGAGTTTGAAGAGCAATTTGGAGTAATTTTTTA	3600	
Qy	3601	CTCATGTTTCGACTTCTGGCAAGGCCATTCACATTTGAGAACTGTGGGATTTAAACCATCTGA	3660	
Db	3601	CTCATGTTTCGACTTCTGGCAAGGCCATTCACATTTGAGAACTGTGGGATTTAAACCATCTGA	3660	
Qy	3661	CCCTAGGCCCAAACTCAGAGAAATGAAATTCCTPAGTGTACTCCATAATGCAACTGTGTAGCCA	3720	
Db	3661	CCCTAGGCCCAAACTCAGAGAAATGGAATTCCTPAGTGTACTCCATAATGCAACTGTGTAGCCA	3720	
Qy	3721	CAGAGTACTTATTCAATTCATTTCCAGATCATCATGAAGGACACTTAACTTTGTTCGAA	3780	
Db	3721	CAGAGTACTTATTCAATTCATTTCCAGATCATCATGAAGGACACTTAACTTTGTTCGAA	3780	
Qy	3781	GCTCTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGGCATGCGAGAGT	3840	
Db	3781	GCTCTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGGCATGCGAGAGT	3840	
Qy	3841	ACGCCATAACCAACGACAGAACCAAGAGGCTGTGGCGCTTCGCACCAAGCACTTTGGCGG	3900	
Db	3841	ACGCCATAACCAACGACAGAACCAAGAGGCTGTGGCGCTTCGCACCAAGCACTTTGGCGG	3900	
Qy	3901	ACCTTTTGGAAATCAATTTATTGCAGCGCTGTGACACTGATAAGGATTTTGGAAATATGTTTCATA	3960	
Db	3901	ACCTTTTGGAAATCAATTTATTGCAGCGCTGTGACACTGATAAGGATTTTGGAAATATGTTTCATA	3960	
Qy	3961	CTTTCATGAATGTCTGCTTCTTTCCACGATTGAAGAAATTCATTTTGAATCAGGATTTGGA	4020	
Db	3961	CTTTCATGAATGTCTGCTTCTTTCCACGATTGAAGAAATTCATTTTGAATCAGGATTTGGA	4020	
Qy	4021	ATGACCCCAAAATCCACGCTTCAGCAGTGTGCTTGACACTTTAGGACAGAGGAAAAGAGC	4080	
Db	4021	ATGACCCCAAAATCCACGCTTCAGCAGTGTGCTTGACACTTTAGGACAGAGGAAAAGAGC	4080	
Qy	4081	CAGACATTCCTCTGTACAAGACTCTGCAGACAGTGGGCCCATCCCATGCCGCAACCTTACA	4140	
Db	4081	CAGACATTCCTCTGTACAAGACTCTGCAGACAGTGGGCCCATCCCATGCCGCAACCTTACA	4140	
Qy	4141	CTGTGGCTGTTTATTTCAAGGGAGAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTTCAGC	4200	
Db	4141	CTGTGGCTGTTTATTTCAAGGGAGAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTTCAGC	4200	
Qy	4201	AAGCGGAAATGGGAGCAGCAATGATCGGCTTGAAATAATATATTTTCCCCAGATGGCCC	4260	
Db	4201	AAGCGGAAATGGGAGCAGCAATGATCGGCTTGAAATAATATATTTTCCCCAGATGGCCC	4260	
Qy	4261	ATCAGAAAGCGGTTTCATCCGAACGGAATGACAGACAAGAGTTTAAAAGAAATCAGAGTGGGAAA	4320	
Db	4261	ATCAGAAAGCGGTTTCATCCGAACGGAATGACAGACAAGAGTTTAAAAGAAATCAGAGTGGGAAA	4320	
Qy	4321	GAGAGCATCAAGAGAGAGAGCCGATCGAGACTGAAGACATCAAGAAATAAGGAGGGGCAT	4380	
Db	4321	GAGAGCATCAAGAGAGAGAGCCGATCGAGACTGAAGACATCAAGAAATAAGGAGGGGCAT	4380	
Qy	4381	GCAAGTGTGAGTATTTACTTGTCTCAGTAACTGTGACTGTGTGTCTATTGTAGACCTAGCCCT	4440	
Db	4381	GCAAGTGTGAGTATTTACTTGTCTCAGTAACTGTGACTGTGTGTCTATTGTAGACCTAGCCCT	4440	
Qy	4441	AGTTTTCTCTGCAGACAAATGAACGAAGTGTGCTCATTTGAAATATAAATACAGAGTCAAAATCG	4500	
Db	4441	AGTTTTCTCTGCAGACAAATGAACGAAGTGTGCTCATTTGAAATATAAATACAGAGTCAAAATCG	4500	
Qy	4501	CTATTGTTGTTTAAATGATCTGTTTTTTAGCTGGATGGTCTTTATTTACAAAGTATTAGATT	4560	

RESULT 4

ADG32900

ID ADG32900 standard; DNA: 4764 BP.

AC ADG32900:

XX
DT 26-FEB-2004 (first entry)XX
DE Human DNA differentially expressed in patients with SLR. SeqID224

human. β_2 : anti-inflammation, chronic inflammation, disease, CRP.

RW human; ds; autoimmune; chronic inflammatory disease; SLE; erythematous lung erythematosis; rheumatoid arthritis; cholelithiasis;

KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
KW Sjogren's disease; erythematous; ankylosing spondylitis;

KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis

KW ulcerative colitis; primary sclerosing cholangitis
 KW diverticulitis; primary biliary sclerosis

XX
05

Homo sapiens

XX
DN
W0300300604-X3

XX
22
23

XX

XX



XX

XX

XX Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
PT colitis, psoriasis and asthma by detecting the expression level of one or
PT more genes.

XX
PS
Claim 18: SEQ ID NO 224: 877bp: English:

This invention relates to novel methods for diagnosing and monitoring autoimmune and chronic inflammatory diseases. Specifically, it refers to the identification of genes that have a clinical utility as diagnostic tools for the management of, in particular, patients with systemic lupus erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the present invention describes a method for determining the levels of multiple differentially expressed genes of a patient, in a concerted manner, in order to achieve an improved diagnostic assay with sensitivity and specificity for the disease in question. As such, these genes are useful for the diagnosis of various other inflammatory disorders including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma, ankylosing spondylitis, ulcerative colitis, primary sclerosing cholangitis, appendicitis, diverticulitis, and primary biliary sclerositis. This polynucleotide is a DNA sequence representing human mRNA that is differentially expressed in patients with SLE, used in an amplification

CC	of the invention.									
XX										
SQ	Sequence 4764 BP; 1379 A; 1138 C; 1082 G; 1165 T; 0 U; 0 Other;									
	Query Match 99.9%; Score 4760.8; DB 10; Length 4764;									
	Best Local Similarity 100.0%; Pred. No. 0;									
	Matches 4762; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	1	CTGTCTTGTG	TACCTCGG	TAGTAC	CGCTTGG	CTCTCTG	ACGGCGAT	CTCTCGG	CCCCGAG	60
DB	1	CTGTCTTGTG	TACCTCGG	TAGTAC	CGCTTGG	CTCTCTG	ACGGCGAT	CTCTCGG	CCCCGAG	60
QY	61	AGCCTTTTAT	AGTTGCT	TTTCCCGGG	ATGTGA	AGGATAC	GAAATG	ACTGTGA	ATCAA	120
DB	61	AGCCTTTTAT	AGTTGCT	TTTCCCGGG	ATGTGA	AGGATAC	GAAATG	ACTGTGA	ATCAA	120
QY	121	CCCATATCAT	CAAGGAG	CTGATA	CTCTAGTGA	AGAGTTAG	ACGTGTG	CATCTTCA	CTA	180
DB	121	CCCATATCAT	CAAGGAG	CTGATA	CTCTAGTGA	AGAGTTAG	ACGTGTG	CATCTTCA	CTA	180
QY	181	TGATATGAGG	CGAGTCT	CTGAGCTT	ATATCTCTGTGA	AGATGTGA	CATATCCAGG	CGGA		240
DB	181	TGATATGAGG	CGAGTCT	CTGAGCTT	ATATCTCTGTGA	AGATGTGA	CATATCCAGG	CGGA		240
QY	241	ACATCATGAT	GCAGGGA	AAACAT	TGTCACAGAA	TGTGCTTCCAC	CGGACGAGG	CGTC		300
DB	241	ACATCATGAT	GCAGGGA	AAACAT	TGTCACAGAA	TGTGCTTCCAC	CGGACGAGG	CGTC		300
QY	301	CCCGAGGAC	GAGGAGG	ACATG	GAGCCAGAC	CCCTCAGCACCAT	CTTTTAGG	CCCCCAATC		360
DB	301	CCCGAGGAC	GAGGAGG	ACATG	GAGCCAGAC	CCCTCAGCACCAT	CTTTTAGG	CCCCCAATC		360
QY	361	TGAGGCTG	CTTCA	CCCTCAG	CAGCGCTCTCTGTG	CAATATCAAT	TGAACCTT	CCAAGT	CCCC	420
DB	361	TGAGGCTG	CTTCA	CCCTCAG	CAGCGCTCTCTGTG	CAATATCAAT	TGAACCTT	CCAAGT	CCCC	420
QY	421	CTTCCACCA	CTTTCTCA	AACTCTCC	AGCCCCCAATTTTCT	CCCTCCACG	ACCAGACT	TTTG		480
DB	421	CTTCCACCA	CTTTCTCA	AACTCTCC	AGCCCCCAATTTTCT	CCCTCCACG	ACCAGACT	TTTG		480
QY	481	TACCTTCCCC	CCACCCAT	CGCTCGG	TGAGCGGAC	GGCCCTCTTCC	CCCCCTG	CCCCATCA		540
DB	481	TACCTTCCCC	CCACCCAT	CGCTCGG	TGAGCGGAC	GGCCCTCTTCC	CCCCCTG	CCCCATCA		540
QY	541	GGCGGCTTT	TCCCAAC	CAAGATG	AGGCAAC	CCCTTCCAGT	TCTCTGTTT	TCTTC		600
DB	541	GGCGGCTTT	TCCCAAC	CAAGATG	AGGCAAC	CCCTTCCAGT	TCTCTGTTT	TCTTC		600
QY	601	CCATGCCAC	CAACCAAT	GTCTTCT	CTAATAA	CCCCCGAGT	CCCTGGGG	CACCTCTG	GCAC	660
DB	601	CCATGCCAC	CAACCAAT	GTCTTCT	CTAATAA	CCCCCGAGT	CCCTGGGG	CACCTCTG	GCAC	660
QY	661	AAGGCACT	TTTCCCTT	CATGATG	CGCCCTCC	CTCATGCT	CTATCCCC	CGGCCCCCT	CCAG	720
DB	661	AAGGCACT	TTTCCCTT	CATGATG	CGCCCTCC	CTCATGCT	CTATCCCC	CGGCCCCCT	CCAG	720
QY	721	TCATGCCG	CAGAGTTA	TATCAGT	ACCTCCGGG	CTATCTCAC	CAACTT	TCCAC		780
DB	721	TCATGCCG	CAGAGTTA	TATCAGT	ACCTCCGGG	CTATCTCAC	CAACTT	TCCAC		780
QY	781	CTCCAGTT	TTTAA	TAGTTTCC	AGAACAC	CCCTAGTTCT	TTTCTG	CCCCAGT	GTCTAATA	840
DB	781	CTCCAGTT	TTTAA	TAGTTTCC	AGAACAC	CCCTAGTTCT	TTTCTG	CCCCAGT	GTCTAATA	840
QY	841	GCAGTAGT	CTCA	TTTTCAG	ACATCTCC	CTCATAC	CCCAAGG	CTCCAGT	GAGA	900
DB	841	GCAGTAGT	CTCA	TTTTCAG	ACATCTCC	CTCATAC	CCCAAGG	CTCCAGT	GAGA	900
QY	901	GAAGTCCC	CAAGAGG	CTGA	ACATATG	ATGACCA	CCAGGAC	CCGAC	CACTAGT	960
DB	901	GAAGTCCC	CAAGAGG	CTGA	ACATATG	ATGACCA	CCAGGAC	CCGAC	CACTAGT	960
QY	961	GGCGAGGT	GAGGCGAT	CGTCT	CTTGGAT	CGGCGGAG	CGGCGG	CAGT	CTCCGAC	1020
DB	961	GGCGAGGT	GAGGCGAT	CGTCT	CTTGGAT	CGGCGGAG	CGGCGG	CAGT	CTCCGAC	1020

Db 2041 ATATCTTTGAAGGATTTTCTATGTTTGACATGCCCCCTGACCAATATTTCCACTGTGTA 2100
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Db 2161 ATTTTGTGTGAAGGCTTGAACCTCTTTTCACTGTTTCCATTTTCATGTAAGAGATATTTTGAAT 2220
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Db 2221 TATATGACTGGAATCTTTAAAGGTCCTTTGTTTGAAGACAGCCCTCCCTGCTGCCCCAAGAT 2280
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DB 841 GCAGTAGTCTCATATTCAGACATCTCCCTCATACCACTCCCAAAGGCTCCCAAGTGAGA 900
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QY 4501 CTATTTGTTTAAATGATCTGTTTTTGTAGTGGATGGTCTTTATTACAAGTATTAGATT 4560
Db 4501 CTATTTGTTTAAATGATCTGTTTTTGTAGTGGATGGTCTTTATTACAAGTATTAGATT 4560
QY 4561 TTTCTCTTATTTAAACGGAACCTTGACTTTGCTGTAATGTCATTTCTCTTTTATTG 4620
Db 4561 TTTCTCTTATTTAAACGGAACCTTGACTTTGCTGTAATGTCATTTCTCTTTTATTG 4620
QY 4621 CTCCTTAAATAATAAAATTCAGAAAGCATATTCTATGTGGAATAGATCCTGTTTTCCAT 4680
Db 4621 CTCCTTAAATAATAAAATTCAGAAAGCATATTCTATGTGGAATAGATCCTGTTTTCCAT 4680
QY 4681 CTGTGCTCCAGATTTGTGACCTTAGACTTTCAATTCAGAAAGTAAAAATTGACTTTACTAG 4740
Db 4681 CTGTGCTCCAGATTTGTGACCTTAGACTTTCAATTCAGAAAGTAAAAATTGACTTTACTAG 4740
QY 4741 TAAAAAATAAAAAAAAAAAAAA 4764
Db 4741 TAAAAAATAAAAAAAAAAAAAA 4764

RESULT 6
ADR68726
ID ADR68726 standard; cDNA; 4764 BP.
XX
AC ADR68726;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human cDNA encoding Ribonuclease III, RNase III.
XX
KW Human; ss; gene; Ribonuclease III; RNase III; RNA interference;
KW gene silencing; double stranded RNA; pre-rRNA processing; RNA processing;
KW RNA expression; RNA splicing; RNA translocation.
OS Homo sapiens.
XX
FH Key
CDS 246..4370
FT /*tag= a
FT /product= "Ribonuclease III"
FT /transl_except= (pos:3876..3878,aa:Gly)
FT /transl_except= (pos:4278..4280,aa:Gly)
XX
PN US2004175828-A1.
```

XX 09-SEP-2004.
PD
XX 22-MAR-2004; 2004US-00805919.
PF
XX 06-JUL-2001; 2001US-00900425.
PR
XX (CROO/) CROOKE S T.
PA (WUHH/) WU H.
XX
XX Crooke ST, Wu H;
PI
XX WPI; 2004-667111/65.
DR
XX Modulating RNA interference, processing, expression, splicing and
PT translation in cell or tissue, by contacting cell or tissue with human
PT RNase III or oligomeric compound targeted to nucleic acid encoding human
PT RNase III.
PT
XX
PS Example 2; SEQ ID NO 1; 32pp; English.
CC
CC The invention relates to modulating RNA interference (gene silencing),
CC RNA processing (e.g. of pre-rRNA), RNA expression, RNA splicing, or RNA
CC translocation in a cell or tissue, by contacting the cell or tissue with
CC a modulator effective to cause the modulation by at least 50% as compared
CC to control, where modulator is human RNase III (ribonuclease III, which
CC cleaves double stranded RNA) polypeptide or an oligomeric compound (an
CC antisense oligonucleotide) targeted to the nucleic acid encoding human
CC RNase III. The oligomeric compound is targeted to a 3'-untranslated
CC region (3'UTR), a 5'-untranslated region (5'UTR) or a coding region of a
CC nucleic acid molecule encoding human RNase III polypeptide, where the
CC oligomeric compound inhibits the expression of human RNase III
CC polypeptide by at least 50%. In the method above, the RNA is rRNA, snRNA,
CC snoRNA or miRNA, or precursors of the above. The RNA is processed to form
CC one or more 30S and 32S RNA fragments. The 32S RNA is processed to form
CC one or more 12S pre-rRNA and 28S RNA fragments. The methods are useful
CC for modulating RNA interference in a cell or tissue, modulating
CC processing of an RNA in a cell or tissue, modulating RNA expression in a
CC cell or tissue, modulating RNA splicing in a cell or tissue, and
CC modulating RNA translocation in a cell or tissue. The methods are useful
CC for research, biological and clinical purposes. The methods are useful in
CC defining the roles of RNase III and interaction of human RNase III and
CC cellular RNA. The present sequence encodes human RNaseIII.
XX
SQ Sequence 4764 BP; 1379 A; 1138 C; 1082 G; 1165 T; 0 U; 0 Other;
Query Match 99.9%; Score 4760.8; DB 13; Length 4764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4762; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGCTCTGGTACCTGCGGTAGTAGCCTGGCTTTGCTCTGACGCGCATCTCGGGCCCGAG 60
DB 1 CTGCTCTGGTACCTGCGGTAGTAGCCTGGCTTTGCTCTGACGCGCATCTCGGGCCCGAG 60
QY 61 AGCTTTTATAGTTGCTTTTCCGGGGATGTGAAGGATACAGAAATGACTGTGAATCAA 120
DB 61 AGCTTTTATAGTTGCTTTTCCGGGGATGTGAAGGATACAGAAATGACTGTGAATCAA 120
QY 121 CCCATATCATCAGGAGCTGTAATCTAGTGAAGAGTTAGACGTGTGCATCTTCACTA 180
DB 121 CCCATATCATCAGGAGCTGTAATCTAGTGAAGAGTTAGACGTGTGCATCTTCACTA 180
QY 181 TGATATGAGGCACTCTCTGAGCTTATATTTCTGTGGAAGATGTGACATATCCAGCGGA 240
DB 181 TGATATGAGGCACTCTCTGAGCTTATATTTCTGTGGAAGATGTGACATATCCAGCGGA 240
QY 241 ACATCATGATGAGGGAACACATGTCA CAGAAATGTGTTTCCACCGGACGAGGCGTC 300
DB 241 ACATCATGATGAGGGAACACATGTCA CAGAAATGTGTTTCCACCGGACGAGGCGTC 300
QY 301 CCCGAGGACGAGGAGACATGGACGAGACCTTCAGCACCATCTTTAGGCCCCCAAAATC 360
DB 301 CCCGAGGACGAGGAGACATGGAGCCAGACCTTCAGCACCATCTTTAGGCCCCCAAAATC 360

QY 361 TGAGGCTGCTTCAACCTCAGCAGCCTCTGTGCAATATCAATATGAACCTCAAGTGCCC 420
DB 361 TGAGGCTGCTTCAACCTCAGCAGCCTCTGTGCAATATCAATATGAACCTCAAGTGCCC 420
QY 421 CTTCCACCACTTTCTCAAACTCTCCAGCCCCCAATTTCTCCCTCCACACAGACTTTG 480
DB 421 CTTCCACCACTTTCTCAAACTCTCCAGCCCCCAATTTCTCCCTCCACACAGACTTTG 480
QY 481 TACCTTTCCCCCAACCCATGCTCCGTGAGCGCAAGGCCCTCTTCCCTCCCAATCA 540
DB 481 TACCTTTCCCCCAACCCATGCTCCGTGAGCGCAAGGCCCTCTTCCCTCCCAATCA 540
QY 541 GGCCTGCTTCCCAACCAACAGATGAGCAGCCCTTCCAGTTCTCTGTTTCTTCTC 600
DB 541 GGCCTGCTTCCCAACCAACAGATGAGCAGCCCTTCCAGTTCTCTGTTTCTTCTC 600
QY 601 CCATGCGCACCAATGCTTGTCTTAATAACCCCCAGTCCCTGGGGCACCTCTCTGGAC 660
DB 601 CCATGCGCACCAATGCTTGTCTTAATAACCCCCAGTCCCTGGGGCACCTCTCTGGAC 660
QY 661 AAGGCATTTTCCCTTTCATGATGCCCTTCTCTCATGCTCATCCCGCCCCCTCCAG 720
DB 661 AAGGCATTTTCCCTTTCATGATGCCCTTCTCTCATGCTCATCCCGCCCCCTCCAG 720
QY 721 TCATCGCGCAGCAGGTTAATATCATGATCCCTCCGGGCTATTTCTACCAACATTTCCCAC 780
DB 721 TCATCGCGCAGCAGGTTAATATCATGATCCCTCCGGGCTATTTCTACCAACATTTCCCAC 780
QY 781 CTCCTCAGTTTAAATAGTTTTCAGAAACACCTTAGTTCTTCTGCCCCAGTGTCTAATAACA 840
DB 781 CTCCTCAGTTTAAATAGTTTTCAGAAACACCTTAGTTCTTCTGCCCCAGTGTCTAATAACA 840
QY 841 GCAGTAGTCTCTCATTTTCAGACATCTCCCTTCCATACCCACTCCCAAGGCTCCCAAGTGA 900
DB 841 GCAGTAGTCTCTCATTTTCAGACATCTCCCTTCCATACCCACTCCCAAGGCTCCCAAGTGA 900
QY 901 GAAGTCTCCCAAGGCTGAAACATATGATGACACAGGACCGAGACACAGTCAATG 960
DB 901 GAAGTCTCCCAAGGCTGAAACATATGATGACACAGGACCGAGACACAGTCAATG 960
QY 961 GCGGAGGTGAGAGGATCGTCCCTTGGATCGCGGGAGCGGCGAGTCCCGACAGGA 1020
DB 961 GCGGAGGTGAGAGGATCGTCCCTTGGATCGCGGGAGCGGCGAGTCCCGACAGGA 1020
QY 1021 GAAAGCAAGACAGCGGTACAGATCTGATTTATGACCGAGGGAGAACACCATCTCGCCACC 1080
DB 1021 GAAAGCAAGACAGCGGTACAGATCTGATTTATGACCGAGGGAGAACACCATCTCGCCACC 1080
QY 1081 GCAGCTACGAAACGAGCAGAGCGAGAACCGGGAGAGACACAGGATCGAGACAAACCGAA 1140
DB 1081 GCAGCTACGAAACGAGCAGAGCGAGAACCGGGAGAGACACAGGATCGAGACAAACCGAA 1140
QY 1141 GATCACCCTCTCTGAAAGGCTCTACAAAGAGATATAAGAGATCTGGAAGAGTTACG 1200
DB 1141 GATCACCCTCTCTGAAAGGCTCTACAAAGAGATATAAGAGATCTGGAAGAGTTACG 1200
QY 1201 GTTTATCGGTTTCTCTGAACTCTGATGACACACAGAAATTTACCTGGGAGATTTATTA 1260
DB 1201 GTTTATCGGTTTCTCTGAACTCTGATGACACACAGAAATTTACCTGGGAGATTTATTA 1260
QY 1261 AAAATACAGATTTCTTGGGCCCCCCTGAGATTTGTGAATCATCGTCTCCCAAGTAGGG 1320
DB 1261 AAAATACAGATTTCTTGGGCCCCCCTGAGATTTGTGAATCATCGTCTCCCAAGTAGGG 1320
QY 1321 AGAAGAGAGAGCTGTTGGGAGGAGAAAGACCGTTGGAGTGACACACAGAGTTCTG 1380
DB 1321 AGAAGAGAGAGCTGTTGGGAGGAGAAAGACCGTTGGAGTGACACACAGAGTTCTG 1380
QY 1381 GCAAGAGACAGAACTATATACCTCAATCAAGGAAAAAGAGCCCGAGGAGACCATGCTGACA 1440
DB 1381 GCAAGAGACAGAACTATATACCTCAATCAAGGAAAAAGAGCCCGAGGAGACCATGCTGACA 1440

1441 AGAATGAGGAGGAAGAAGAACTTTCTTAAGCCTGTGTGGATTTCGATGCATCTCAATTGAC 1500
1441 AGAATGAGGAGGAGGAAGAAGAACTTTCTTAAGCCTGTGTGGATTTCGATGCATCTCAATTGAC 1500
1501 AAAAATTAATCTCACTGAGTACCCCATGGATCAGGTGGGAGATTCTACAGTGGTTGGAAACGA 1560
1501 AAAAATTAATCTCACTGAGTACCCCATGGATCAGGTGGGAGATTCTACAGTGGTTGGAAACGA 1560
1561 GTAGGCTTCGTGACTTATATGACAAATTTGAGGAGGAGTTGGGGAGCGAGGCAAGAAAGG 1620
1561 GTAGGCTTCGTGACTTATATGACAAATTTGAGGAGGAGTTGGGGAGCGAGGCAAGAAAGG 1620
1621 CCAAGCTGCTCGGCCCTCGTGGGAACCTCCAAAGACGAAGCTTCGATGAAGATTTTAGAGA 1680
1621 CCAAGCTGCTCGGCCCTCGTGGGAACCTCCAAAGACGAAGCTTCGATGAAGATTTTAGAGA 1680
1681 GTTCCAGTGAATCCGAGTGTGAGTGTGATGAGGACAGCACCTGTTCTAGCAGCTCAGACT 1740
1681 GTTCCAGTGAATCCGAGTGTGAGTGTGATGAGGACAGCACCTGTTCTAGCAGCTCAGACT 1740
1741 CTGAACTTTTGAAGTTATGCGAATCANAAAGGCGAAGGCGCCACCTGACCGACTTC 1800
1741 CTGAACTTTTGAAGTTATGCGAATCANAAAGGCGAAGGCGCCACCTGACCGACTTC 1800
1801 ATGATGAACTTTGGTACAAAGATCCAGGCGCAGATGAATGATGACCACTCTGCAAAATGCA 1860
1801 ATGATGAACTTTGGTACAAAGATCCAGGCGCAGATGAATGATGACCACTCTGCAAAATGCA 1860
1861 GCGCAAGGCAAGACGCAAGGAAATTTAGGCAAGCAATTTATCTGAGGAAGAGGCCATCA 1920
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1921 AGCCCTGTGCTCTATGACCAAACTGCTGGGACACTTTTCCACTACCGGATCAGACTCT 1980
1921 AGCCCTGTGCTCTATGACCAAACTGCTGGGACACTTTTCCACTACCGGATCAGACTCT 1980
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1981 CCCCGCTACGAACTTTTAACTGACAGGCAACTGTTATAGAAATACGATGATCAGAGT 2040
2041 ATATCTTTGAAGGATTTCTATGTTTGCACATGCCGCCCTGACCAATATTTCACTGTGTA 2100
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2161 ATTTTGTGTGAAGGGCTTGAACCTCTTTTCACTGTTCTTATTCAGAGATATTTTGGAAAT 2220
2221 TATATGACTGGAATCTTAAAGGTCCTTTGTTGAAGACAGCCCTCCCTGCTGCCCAAGAT 2280
2221 TATATGACTGGAATCTTAAAGGTCCTTTGTTGAAGACAGCCCTCCCTGCTGCCCAAGAT 2280
2281 TTCAATTTTCATGCCAGCTTTTGAAGATTTCTCCAGATGGAGAAAGGAGTCTGTCCA 2340
2281 TTCAATTTTCATGCCAGCTTTTGAAGATTTCTCCAGATGGAGAAAGGAGTCTGTCCA 2340
2341 TGCACAGATTTCTCTGTACTCTGTTAAGGTGACAGAAAGCCCTGCTGAGGAGGAGA 2400
2341 TGCACAGATTTCTCTGTACTCTGTTAAGGTGACAGAAAGCCCTGCTGAGGAGGAGA 2400
2401 TTGCCAATATGCTTCAGTGGGAGGAGCTGGAGTGGCAGAAATATGAGAAAGATGCAAAAG 2460
2401 TTGCCAATATGCTTCAGTGGGAGGAGCTGGAGTGGCAGAAATATGAGAAAGATGCAAAAG 2460
2461 GCATGATTTGTACCAACCCCTGGGACGAAACCAAGCTCTGTCCGTATCGATCAACTGGATC 2520
2461 GCATGATTTGTACCAACCCCTGGGACGAAACCAAGCTCTGTCCGTATCGATCAACTGGATC 2520
2521 GTGAACAGTTTCAACCCCGATGTGATTACTTTTCCGATTAATCGTCCACTTTTGGGATACGCC 2580

2521 GTGAACAGTTTCAACCCCGATGTGATTACTTTTCCGATTAATCGTCCACTTTGGGATACGCC 2580
2581 CTGCAAGTTGAGTTTATCGAGGAGACCCACAGTACCAAAAATCTGTGGAGAGATTATGTGA 2640
2581 CTGCAAGTTGAGTTTATCGAGGAGACCCACAGTACCAAAAATCTGTGGAGAGATTATGTGA 2640
2641 AACTTTCGCACCTCTAGCAAAATAGTCCCAAAAGTCAAAACAAACTGACAAAAGAAAGCTGG 2700
2641 AACTTTCGCACCTCTAGCAAAATAGTCCCAAAAGTCAAAACAAACTGACAAAAGAAAGCTGG 2700
2701 CACAGAGGAGGAAGCCCTCCAAAAAATACGCGAGAAGAATAAATGACAGAGAAAGTAA 2760
2701 CACAGAGGAGGAAGCCCTCCAAAAAATACGCGAGAAGAATAAATGACAGAGAAAGTAA 2760
2761 CGGTGGAGTAAGTAGCCAAAGGATTTCTGAAAACCTGGCAATCCGTTCTGATGCTGTGACG 2820
2761 CGGTGGAGTAAGTAGCCAAAGGATTTCTGAAAACCTGGCAATCCGTTCTGATGCTGTGACG 2820
2821 ATGCAATGATGCTACTGTTCTGACCCCATCATATCCGCTTACCAACCAATGCCTAAATGCAAT 2880
2821 ATGCAATGATGCTACTGTTCTGACCCCATCATATCCGCTTACCAACCAATGCCTAAATGCAAT 2880
2881 TGGACAAGTTGATAGATATATCTTTCCAAAGATCGTTGTCTGTTGCAAGCTGGCCATGACTC 2940
2881 TGGACAAGTTGATAGATATATCTTTCCAAAGATCGTTGTCTGTTGCAAGCTGGCCATGACTC 2940
2941 ATCCAAGTCATCATTTAAATTTTGGAAATGAAATCCCTGATCATGCCAGGAATTCATTAICTA 3000
2941 ATCCAAGTCATCATTTAAATTTTGGAAATGAAATCCCTGATCATGCCAGGAATTCATTAICTA 3000
3001 ACTGTGGAATTCGGCAGGCCAAATACGGAGACAGAAAAAGTTTCATCACATGCACATCGGA 3060
3001 ACTGTGGAATTCGGCAGGCCAAATACGGAGACAGAAAAAGTTTCATCACATGCACATCGGA 3060
3061 AGAAAAGGATTAACACCTTTGATAAATATCATGTACGCTTGGCCCAAGATGACCCAACTC 3120
3061 AGAAAAGGATTAACACCTTTGATAAATATCATGTACGCTTGGCCCAAGATGACCCAACTC 3120
3121 CCTCGAGGATTAACCAATGAACGGTTGGAATTCCTGGGTGATGCTGTTGTTGAATTC 3180
3121 CCTCGAGGATTAACCAATGAACGGTTGGAATTCCTGGGTGATGCTGTTGTTGAATTC 3180
3181 TGACACAGCTCCATTTGTACTATTTGTTTCTAGTCTGGAAGAAGAGAGATTAGCAACCT 3240
3181 TGACACAGCTCCATTTGTACTATTTGTTTCTAGTCTGGAAGAAGAGAGATTAGCAACCT 3240
3241 ATCGGACTGCCATTTGTTCAAGATCAGACCTTTGCCATGCTAGCAAAAGAACTTTGAACCTGG 3300
3241 ATCGGACTGCCATTTGTTCAAGATCAGACCTTTGCCATGCTAGCAAAAGAACTTTGAACCTGG 3300
3301 ATCCATTTATGCTGATGCTCAGGGCCCTGACCTTTGTAGAGAACTCGGACCTTCGACATG 3360
3301 ATCCATTTATGCTGATGCTCAGGGCCCTGACCTTTGTAGAGAACTCGGACCTTCGACATG 3360
3361 CAATGCCAAATTTGTTTGAAGCGTTAAATAGGAGCTGTTTACTTTGAGGGAAGCCTCGAGG 3420
3361 CAATGCCAAATTTGTTTGAAGCGTTAAATAGGAGCTGTTTACTTTGAGGGAAGCCTCGAGG 3420
3421 AAGCCAAAGCAGTTATTTGGACGCTTCTCTTAAATGATCCGGACCTTCGCGAAGTCTGGC 3480
3421 AAGCCAAAGCAGTTATTTGGACGCTTCTCTTAAATGATCCGGACCTTCGCGAAGTCTGGC 3480
3481 TCATTTATCTCTCCACCCACTCCAACTACAGGCCAAATACTGATCCGAACTTTATTG 3540
3481 TCATTTATCTCTCCACCCACTCCAACTACAGGCCAAATACTGATCCGAACTTTATTG 3540
3541 AAACTTCTCCAGTTCTACAAAAAATTTACTGAGTTTGAAGAAGCAATTTGAGTAATTTTAA 3600
3541 AAACTTCTCCAGTTCTACAAAAAATTTACTGAGTTTGAAGAAGCAATTTGAGTAATTTTAA 3600
3601 CTCATGTTTCGACTTCTGGCAAGGCCATTCATTAATGAGAACTGTGGGATTTAACCATCTGA 3660
3601 CTCATGTTTCGACTTCTGGCAAGGCCATTCATTAATGAGAACTGTGGGATTTAACCATCTGA 3660

Db 3601 CTGATGTTGACTTCTGCGAAGGCAATTCACATTTGAGAACTGTGGGATTTAACCATCTGA 3660
Qy 3661 CCTAGGCCCAATCAGAGAAATGGAATTCCTAGGTGATCCATAATGCAACTGTGTAGCCA 3720
Db 3661 CCTAGGCCCAATCAGAGAAATGGAATTCCTAGGTGATCCATAATGCAACTGTGTAGCCA 3720
Qy 3721 CAGAGTACTTATTCAATTCATTTCCAGATCATCATGAGGACACTTAACTTTGTTCGAA 3780
Db 3721 CAGAGTACTTATTCAATTCATTTCCAGATCATCATGAGGACACTTAACTTTGTTCGAA 3780
Qy 3781 GCTCTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGCGATCGAGGAT 3840
Db 3781 GCTCTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGCGATCGAGGAT 3840
Qy 3841 ACGCCATAACAACGACAAGCAAGAGGCTGTGGCGCTTCGCAACAGACCTTGGCGG 3900
Db 3841 ACGCCATAACAACGACAAGCAAGAGGCTGTGGCGCTTCGCAACAGACCTTGGCGG 3900
Qy 3901 ACCTTTTGGATCATTTATTGCGAGCGCTGTACACTGATAGGATTTTGGAAATATGTCATA 3960
Db 3901 ACCTTTTGGATCATTTATTGCGAGCGCTGTACACTGATAGGATTTTGGAAATATGTCATA 3960
Qy 3961 CTTTCATGAATGTCTGCTCTTTCCAGATTTGAAGAAATTCATTTGAATCAGGATTTGA 4020
Db 3961 CTTTCATGAATGTCTGCTCTTTCCAGATTTGAAGAAATTCATTTGAATCAGGATTTGA 4020
Qy 4021 ATGACCCCAATCCAGCTTTCAGCAGTGTGCTTGACACTTAGGACAGAGAAAGAGC 4080
Db 4021 ATGACCCCAATCCAGCTTTCAGCAGTGTGCTTGACACTTAGGACAGAGAAAGAGC 4080
Qy 4081 CAGACATTCCTGTACAGACTCTGCAGACAGTGGGCCCATCCCATGCCCGAACCTACA 4140
Db 4081 CAGACATTCCTGTACAGACTCTGCAGACAGTGGGCCCATCCCATGCCCGAACCTACA 4140
Qy 4141 CTGTGGCTGTTTATTTCAAGGAGAAAGATAGCTGTGGGAAAGACCAAGTATTTCAGC 4200
Db 4141 CTGTGGCTGTTTATTTCAAGGAGAAAGATAGCTGTGGGAAAGACCAAGTATTTCAGC 4200
Qy 4201 AAGCGGAAATGGGAGCAGCAATGATGCGCTTGAAATAATATTTTCCACAGATGCC 4260
Db 4201 AAGCGGAAATGGGAGCAGCAATGATGCGCTTGAAATAATATTTTCCACAGATGCC 4260
Qy 4261 ATCAGAAGCGGTTTCATCGAAGCAAGTACAGACAGAGTTTAAAGAAATGAGTGGGAA 4320
Db 4261 ATCAGAAGCGGTTTCATCGAAGCAAGTACAGACAGAGTTTAAAGAAATGAGTGGGAA 4320
Qy 4321 GAGAGCATCAAGAGAGAGCCAGATGAGACTGAGACATCAAGAAATAAAGGAGGSCAT 4380
Db 4321 GAGAGCATCAAGAGAGAGCCAGATGAGACTGAGACATCAAGAAATAAAGGAGGSCAT 4380
Qy 4381 GCAAGTGTGGAGTATTTACTTGTCTCAGTAACTGTGACTGTGTCTATTGAGACCTAGCCT 4440
Db 4381 GCAAGTGTGGAGTATTTACTTGTCTCAGTAACTGTGACTGTGTCTATTGAGACCTAGCCT 4440
Qy 4441 AGTTTTCCTGACAGCAATGAACGAGTGTCTCATTTGAATAAATAACAGAGTCAATCG 4500
Db 4441 AGTTTTCCTGACAGCAATGAACGAGTGTCTCATTTGAATAAATAACAGAGTCAATCG 4500
Qy 4501 CTATTGTTGTTTAAATGATCTGTTTGTAGCTGATGCTTTTATTACAAAGTATTAGATT 4560
Db 4501 CTATTGTTGTTTAAATGATCTGTTTGTAGCTGATGCTTTTATTACAAAGTATTAGATT 4560
Qy 4561 TTTCTTCTATTAAACGGAAATCTGACTTTGGTGAATGTGCATTACTCTCTTTTATTG 4620
Db 4561 TTTCTTCTATTAAACGGAAATCTGACTTTGGTGAATGTGCATTACTCTCTTTTATTG 4620
Qy 4621 CTCTTTAAATATAAATCAAGAGCATATTTATGTGGAATAGATCTCTGTTTTCAT 4680
Db 4621 CTCTTTAAATATAAATCAAGAGCATATTTATGTGGAATAGATCTCTGTTTTCAT 4680
Qy 4681 CTGTGTCAGATGTGACCCCTAGACTTTCATTTGCAAGTAAATAATGACTTTACTAG 4740
Db 4681 CTGTGTCAGATGTGACCCCTAGACTTTCATTTGCAAGTAAATAATGACTTTACTAG 4740

Qy 4741 TAAAAA 4764
Db 4741 TAAAAA 4764

RESULT 7

ADX03768
ID ADX03768 standard; cDNA; 4764 BP.

XX ADX03768;

AC AC

DT 05-MAY-2005 (first entry)

XX Human cDNA encoding Drosha RNase III.

DE Drosha; RNase III; RNA interference; gene silencing; Cytostatic;
XX Antidiabetic; Anorectic; Antilipemic; Antiarteriosclerotic; Hypotensive;
KW Neuroprotective; Nootropic; Antiangiogenic; Anabolic;
KW Eating-Disorders-Gen.; hyperproliferation; cancer; neoplasm;
KW angiogenesis disorder; cardiovascular disease;
KW non-insulin dependent diabetes; endocrine disease;
KW gastrointestinal disease; metabolic disorder; obesity;
KW nutritional disorder; hyperlipidemia; atherosclerosis; atherogenesis;
KW hypertension; anorexia nervosa; nutritional disorder;
KW psychiatric disorder; Alzheimers disease; degeneration;
KW neurological disease; nervous system injury; neurodegenerative disease;
KW neurological disorder; gene; ss.

OS Homo sapiens.

XX WO2005013901-A2.

PN 17-FEB-2005.

XX 30-JUL-2004; 2004WO-US025300.

XX 31-JUL-2003; 2003US-0492056P.

PR 31-OCT-2003; 2003US-0516303P.

PR 19-DEC-2003; 2003US-0531596P.

PR 14-APR-2004; 2004US-0562417P.

XX (ISIS-) ISIS PHARM INC.

XX Esau C, Lollo B, Bennett CF, Freier SM, Griffey RH, Baker BF;

PI Vickers T, Marcussen EG, Koller E, Swayze EE, Jain R, Bhat B;

PI Peralta E;

XX WPI; 2005-163123/17.

XX Example 24; SEQ ID NO 860; 854pp; English.

PT New oligomeric compound that can hybridize with or sterically interfere
PT with nucleic acid molecules comprising or encoding small non-coding RNA
PT targets, useful for treating e.g., cancer and diabetes.
XX
XX The invention relates to an oligomeric compound comprising a first region
CC and a second region, where at least one region contains a modification,
CC and a portion of the oligomeric compound is targeted to a small non-
CC coding RNA target nucleic acid that is miRNA (micro-RNA), or its
CC precursor (primary-miRNA, pri-miRNA). Also included are a composition
CC comprising a first oligomeric compound and a second oligomeric compound
CC (where at least one of the oligomeric compounds contains a modification,
CC at least a portion of the first oligomeric compound is capable of
CC hybridizing with at least a portion of the second oligomeric compound,
CC and at least a portion of the first oligomeric compound is targeted to a
CC small non-coding RNA target nucleic acid, a pharmaceutical composition
CC comprising the composition cited above (and a carrier), a kit or assay
CC device comprising the composition, modulating the expression of a small
CC non-coding RNA target nucleic acid in a cell (or tissue or animal),
CC treating or preventing a disease or disorder associated with a small non-
CC coding RNA target nucleic acid, treating a condition in an animal,
CC treating or preventing a disease or disorder associated with CD36,

CC methods of screening an oligomeric compound for an effect on miRNA
CC signaling, methods of screening a miRNA precursor for an effect in miRNA
CC signaling, methods of modulating translation (or apoptosis, conversion of
CC a precursor miRNA into miRNA, or cellular differentiation), identifying
CC an RNA transcript bound to a small non-coding RNA, arresting (or
CC delaying) entry of a cell at the G2/M phase, interfering with chromosome
CC segregation, a method of triggering apoptosis, detecting a miRNA
CC precursor, identifying a miRNA target, modulating cellular
CC differentiation, treating a condition associated with adipocyte
CC differentiation in an animal, treating/preventing a disease/disorder
CC associated with aberrant regulation of the cell cycle by miRNAs,
CC maintaining a pluripotent stem cell and identifying a small non-coding
CC RNA binding site. The oligomeric compound is targeted to a region
CC flanking a Drosha cleavage site within a pri-miRNA. It stimulates an
CC increase in expression of a pri-miRNA. The compounds and compositions are
CC useful for treating a disease or disorder resulting from chromosomal non-
CC disjunction, altered methylation, acetylation, or pseudouridylation state
CC of chromosomes, such as a hyperproliferative condition (e.g. cancer,
CC neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity,
CC hyperlipidemia, atherosclerosis, atherogenesis, hypertension, anorexia,
CC Alzheimer's disease, a central nervous system injury or neurodegenerative
CC disorder. The present sequence is a cDNA representing the Drosha gene, an
CC RNase III that processes pri-miRNA into 70bp pre-miRNA (subsequently
CC processed to miRNA by Dicer RNase).

XX
SQ Sequence 4764 BP; 1379 A; 1138 C; 1082 G; 1165 T; 0 U; 0 Other;

Query Match 99.9%; Score 4760.8; DB 14; Length 4764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4762; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTTGTGACCTCGGTAGTACCTGGCTTTCCTGACGCGCATCTCGGCGCCGAG 60
DB 1 CTGCTTGTGACCTCGGTAGTACCTGGCTTTCCTGACGCGCATCTCGGCGCCGAG 60

QY 61 AGCCTTTTATAGTGTCTTTCCTCGGCGATGTGAAGATACAGAAATGACTGTGAATCAA 120
DB 61 AGCCTTTTATAGTGTCTTTCCTCGGCGATGTGAAGATACAGAAATGACTGTGAATCAA 120

QY 121 CCATATCATCAAGGAGCTGATATCTAGTGAAGAGTTAGCGTGTGCATCTCACTA 180
DB 121 CCATATCATCAAGGAGCTGATATCTAGTGAAGAGTTAGCGTGTGCATCTCACTA 180

QY 181 TGATATGAGCGCTCTGAGCTTATATCTCTGTGGAAGATGTGACATATCCAGCGGA 240
DB 181 TGATATGAGCGCTCTGAGCTTATATCTCTGTGGAAGATGTGACATATCCAGCGGA 240

QY 241 ACATCATGATGACGGGAAACACATGTACAGAAATGTCTTCCACCGGACGAGGCGTC 300
DB 241 ACATCATGATGACGGGAAACACATGTACAGAAATGTCTTCCACCGGACGAGGCGTC 300

QY 301 CCGGAGACGAGGAGACATGAGGACGACCTTCAGACCATCTTTAGGCCCCCAAAATC 360
DB 301 CCGGAGACGAGGAGACATGAGGACGACCTTCAGACCATCTTTAGGCCCCCAAAATC 360

QY 361 TGAGGCTGCTTCACTCCAGCGCTCTGTCGAATATCAATATGAACCTTCCAAAGTGCCC 420
DB 361 TGAGGCTGCTTCACTCCAGCGCTCTGTCGAATATCAATATGAACCTTCCAAAGTGCCC 420

QY 421 CTTTCCACCACTTTCTCAAACTCTCCAGCCCCCAATTTTCTCCCTCCACGACGACTTTG 480
DB 421 CTTTCCACCACTTTCTCAAACTCTCCAGCCCCCAATTTTCTCCCTCCACGACGACTTTG 480

QY 481 TACCTTTCCCCCAACCCATGCTCGTTCAGGCGAAGCGCTCTTCCCTCCCTGCCCATAATCA 540
DB 481 TACCTTTCCCCCAACCCATGCTCGTTCAGGCGAAGCGCTCTTCCCTCCCTGCCCATAATCA 540

QY 541 GGCCTGCTTCCCAACCCATGCTCGTTCAGGCGAAGCGCTCTTCCCTGCTTTTCCCTC 600
DB 541 GGCCTGCTTCCCAACCCATGCTCGTTCAGGCGAAGCGCTCTTCCCTGCTTTTCCCTC 600

QY 601 CCATGCCACCAACCAATGCTTGTCTTAATAACCCCGAGTCCCTGGGCGACCTCTGGAC 660
DB 601 CCATGCCACCAACCAATGCTTGTCTTAATAACCCCGAGTCCCTGGGCGACCTCTGGAC 660

DB 601 CCATGCCACCAACCAATGCTTGTCTTAATAACCCCGAGTCCCTGGGCGACCTCTGGAC 660
QY 661 AAGGCACCTTTCCCTTCATGATGCCCTCCCTCCCTCATGCTCATCCCCCGCCCTCCAG 720
DB 661 AAGGCACCTTTCCCTTCATGATGCCCTCCCTCCCTCATGCTCATCCCCCGCCCTCCAG 720
QY 721 TCATGCCGAGCAGGTTAATATCATAGTACCTCCCGGCTTATCTACCACAACTTCCCAC 780
DB 721 TCATGCCGAGCAGGTTAATATCATAGTACCTCCCGGCTTATCTACCACAACTTCCCAC 780
QY 781 CTCCTCAGTTTAAATAGTTTCAGAACCACTAGTTCTTCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 CTCCTCAGTTTAAATAGTTTCAGAACCACTAGTTCTTCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 GCAGTAGTCTCTCAATTCAGACATCTCCCTCCATACCCACTCCCAAGGCTCCCAAGTGA 900
DB 841 GCAGTAGTCTCTCAATTCAGACATCTCCCTCCATACCCACTCCCAAGGCTCCCAAGTGA 900
QY 901 GAAGGTCCCGAAGGCTGAAACATATGATGACACAGGACCGAGACCAAGTCATG 960
DB 901 GAAGGTCCCGAAGGCTGAAACATATGATGACACAGGACCGAGACCAAGTCATG 960
QY 961 GCGAGGTGAGAGGCAATCGTCCCTGGATCGGCGGAGGCGGCGGCTCCCGACAGA 1020
DB 961 GCGAGGTGAGAGGCAATCGTCCCTGGATCGGCGGAGGCGGCGGCTCCCGACAGA 1020
QY 1021 GAAGCAAGACAGCGGTACAGATCTGATTATGACCGAGGAGAACACCATCTCGGCACC 1080
DB 1021 GAAGCAAGACAGCGGTACAGATCTGATTATGACCGAGGAGAACACCATCTCGGCACC 1080
QY 1081 GCAGCTTACGAACCGAGCGAGACGAGAACCGGAGAGACACAGGATCGAGACCAACCGAA 1140
DB 1081 GCAGCTTACGAACCGAGCGAGACGAGAACCGGAGAGACACAGGATCGAGACCAACCGAA 1140
QY 1141 GATCACCATTCTCTGGAAGGCTCTCAAAAAGAGTATGAAGATCTGGAAGGAGTTACG 1200
DB 1141 GATCACCATTCTCTGGAAGGCTCTCAAAAAGAGTATGAAGATCTGGAAGGAGTTACG 1200
QY 1201 GTTTATCGGTCTCTGGAACCTGTGGATGCACACAGAAATTACCTGGGAGATTATTA 1260
DB 1201 GTTTATCGGTCTCTGGAACCTGTGGATGCACACAGAAATTACCTGGGAGATTATTA 1260
QY 1261 AAAATAACAGATCTTTGGGCCCCACCTCGGAGATTGTGAATCATCTCTCCCAAGTAGG 1320
DB 1261 AAAATAACAGATCTTTGGGCCCCACCTCGGAGATTGTGAATCATCTCTCCCAAGTAGG 1320
QY 1321 AGAAGAGAGAGCTCGTTGGGAGGAGAAAAGACCGTTGGAGTGACACACAGAGTTCTG 1380
DB 1321 AGAAGAGAGAGCTCGTTGGGAGGAGAAAAGACCGTTGGAGTGACACACAGAGTTCTG 1380
QY 1381 GCAAGACAGAACTATATCTCAATCAAGGAAAAAGAGCCGAGAGAGACATGCTCTGACA 1440
DB 1381 GCAAGACAGAACTATATCTCAATCAAGGAAAAAGAGCCGAGAGAGACATGCTCTGACA 1440
QY 1441 AGAATGAGGAGGAGAAAGAACTCTTTAAGCTGTGTGGATTTCGATCCATCTCATTCAG 1500
DB 1441 AGAATGAGGAGGAGAAAGAACTCTTTAAGCTGTGTGGATTTCGATCCATCTCATTCAG 1500
QY 1501 AAAAATCTACTCTCAGTGACCCCATGGATCAGGTGGGAGATTCTACAGTGGTGGAAACGA 1560
DB 1501 AAAAATCTACTCTCAGTGACCCCATGGATCAGGTGGGAGATTCTACAGTGGTGGAAACGA 1560
QY 1561 GTAGGCTTCTGACTTATATGACAAATTTGAGAGGAGTTGGGAGCAGGCAAGAAAGG 1620
DB 1561 GTAGGCTTCTGACTTATATGACAAATTTGAGAGGAGTTGGGAGCAGGCAAGAAAGG 1620
QY 1621 CCAAAGCTCTCGGCTCCGTTGGGAACTCCAAAGACGAAGCTCGATGAAGATTATAGAGA 1680
DB 1621 CCAAAGCTCTCGGCTCCGTTGGGAACTCCAAAGACGAAGCTCGATGAAGATTATAGAGA 1680
QY 1681 GTTTCAGTGAATCCGAGTGTGAGTGTGATGAGGACGACCTGTCTTAGCAGCTCAGACT 1740
DB 1681 GTTTCAGTGAATCCGAGTGTGAGTGTGATGAGGACGACCTGTCTTAGCAGCTCAGACT 1740

QY	1741	CTGAAGTTTTGACGTTATTCAGAAATCAAACGCAAAAGGCCACCCCTGACCGACTTC	1800
DB	1741		
QY	1801	ATGATCAACTTTGGTAAACAGATCCAGGCGCAGATGAATGATGACCACTCTCGCAATGCA	1860
DB	1801		
QY	1861	GGCAAAAGCAAGACGCA CAGGAATTTAGGCACAGCACTTTTCCACTACCGGATCACAGTCT	1980
DB	1861		
QY	1921	AGCCCTGTCGTCTATGACCAACAAATGCTGGCAGACTTTTCCACTACCGGATCACAGTCT	1980
DB	1921	AGCCCTGTCGTCTATGACCAACAAATGCTGGCAGACTTTTCCACTACCGGATCACAGTCT	1980
QY	1981	CCCCGCTACGAACTTTTAACTGACAGCGCCAACTGTTATAGAAATACGATGATCAGAGT	2040
DB	1981	CCCCGCTACGAACTTTTAACTGACAGCGCCAACTGTTATAGAAATACGATGATCAGAGT	2040
QY	2041	ATATCTTCAAGGATTTTCTATGTTTGCATATGCCCTCCCTGACCAATATTCACATGTGTA	2100
DB	2041	ATATCTTCAAGGATTTTCTATGTTTGCATATGCCCTCCCTGACCAATATTCACATGTGTA	2100
QY	2101	AAGTAATTAGATTCACATAGACTACAGATTCATTTCAATTGAAGAGATGATGCCGGAGA	2160
DB	2101	AAGTAATTAGATTCACATAGACTACAGATTCATTTCAATTGAAGAGATGATGCCGGAGA	2160
QY	2161	ATTTTGTGCGAAAGGCTTGAACCTTTTCACTGTTCTCTATTTCAGAGATATTTTGGAAAT	2220
DB	2161	ATTTTGTGCGAAAGGCTTGAACCTTTTCACTGTTCTCTATTTCAGAGATATTTTGGAAAT	2220
QY	2221	TATATGACTGGAATCTTAAAGGTCCTTGTGTTGAAGACAGCCCTCCCTGCTGCCCAAGAT	2280
DB	2221	TATATGACTGGAATCTTAAAGGTCCTTGTGTTGAAGACAGCCCTCCCTGCTGCCCAAGAT	2280
QY	2281	TTCAATTTGATGCAAGTTTGAAGATTTCTTCCAGATGAGAGAAAGGAAGTGTGTCCA	2340
DB	2281	TTCAATTTGATGCAAGTTTGAAGATTTCTTCCAGATGAGAGAAAGGAAGTGTGTCCA	2340
QY	2341	TGCACAGATTTCTCTGTACTTGTAAAGTGCAGCAAAAGCCCTGTGCTGAGGAGGAGA	2400
DB	2341	TGCACAGATTTCTCTGTACTTGTAAAGTGCAGCAAAAGCCCTGTGCTGAGGAGGAGA	2400
QY	2401	TTGCCAATATGCTTCAGTGGGAGGAGCTGGAGTGGCAGAAATATGACGAAGAAATGCAAG	2460
DB	2401	TTGCCAATATGCTTCAGTGGGAGGAGCTGGAGTGGCAGAAATATGACGAAGAAATGCAAG	2460
QY	2461	GCAATGATTTTACCAACCTGGGACGAAACCAAGCTCTGTCCGTATCGATCAACTGGATC	2520
DB	2461	GCAATGATTTTACCAACCTGGGACGAAACCAAGCTCTGTCCGTATCGATCAACTGGATC	2520
QY	2521	GTGAAACAGTTCAACCCCGATGTATCTTTTCCGATATCTGCTCCACTTTGGGATACGCC	2580
DB	2521	GTGAAACAGTTCAACCCCGATGTATCTTTTCCGATATCTGCTCCACTTTGGGATACGCC	2580
QY	2581	CTGCAAGTTGAGTTATGACGAGAGCCACAGTACCAAAAACTGTGGAAAGATTATGTA	2640
DB	2581	CTGCAAGTTGAGTTATGACGAGAGCCACAGTACCAAAAACTGTGGAAAGATTATGTA	2640
QY	2641	AACTTGGCCACTCTCTAGCAAAATAGTCCAAAGTCAAAACAACTGACAAACAGAAAGTGG	2700
DB	2641	AACTTGGCCACTCTCTAGCAAAATAGTCCAAAGTCAAAACAACTGACAAACAGAAAGTGG	2700
QY	2701	CACAGAGGAGGAGGAGGCTTCAAAAAATACGCGAGAGAAATCAATGACAGAGAAATTA	2760
DB	2701	CACAGAGGAGGAGGAGGCTTCAAAAAATACGCGAGAGAAATCAATGACAGAGAAATTA	2760
QY	2761	CGGTGAGCTAAGTAGCAAGGATTTCTGAAACTGGCACTCGTTCTGATGCTGTGCAGC	2820
DB	2761	CGGTGAGCTAAGTAGCAAGGATTTCTGAAACTGGCACTCGTTCTGATGCTGTGCAGC	2820

QY	2821	ATGCAATGATGCTACTCTGTTCTGACCCATCATATCGCTACCACTAATGCTTAATGCAATT	2880
DB	2821	ATGCAATGATGCTACTCTGTTCTGACCCATCATATCGCTACCACTAATGCTTAATGCAATT	2880
QY	2881	TGCACAAGTTGATAGGATATCTTTTCCAAAGATCGTTGTCTGTGCAAGCTGGCCATGACTC	2940
DB	2881	TGCACAAGTTGATAGGATATCTTTTCCAAAGATCGTTGTCTGTGCAAGCTGGCCATGACTC	2940
QY	2941	ATCCAAGTCACTATTTAAATTTTGGAAATGAAATCTCTGATCATGCGCAGAAATTCATTATCTA	3000
DB	2941	ATCCAAGTCACTATTTAAATTTTGGAAATGAAATCTCTGATCATGCGCAGAAATTCATTATCTA	3000
QY	3001	ACTGTGGAATTCGGCAGCCCAATACGGAGACAGAAAAGTTTCATCATGCAATGCAATCGGA	3060
DB	3001	ACTGTGGAATTCGGCAGCCCAATACGGAGACAGAAAAGTTTCATCATGCAATGCAATCGGA	3060
QY	3061	AGAAAAGGATTAACACCTTTGATAAAATATCATGTACAGCCCTTGGCCCAAGATGACCAACTC	3120
DB	3061	AGAAAAGGATTAACACCTTTGATAAAATATCATGTACAGCCCTTGGCCCAAGATGACCAACTC	3120
QY	3121	CCTCGAGGATTAACCAATGAAACGGTTGGAAATTTCTCTGGGTGATGCTGTTGTAATTTTC	3180
DB	3121	CCTCGAGGATTAACCAATGAAACGGTTGGAAATTTCTCTGGGTGATGCTGTTGTAATTTTC	3180
QY	3181	TGACCAAGCTCCATTTGTACTATTTGTTTCTAGTCTGGAAGAGGAGATTTAGCAACCT	3240
DB	3181	TGACCAAGCTCCATTTGTACTATTTGTTTCTAGTCTGGAAGAGGAGATTTAGCAACCT	3240
QY	3241	ATCGGACTGCCATTTGTTCAGAAATCAGCACTTGCATGCTAGCAAAAGAACTTTGAACCTGG	3300
DB	3241	ATCGGACTGCCATTTGTTCAGAAATCAGCACTTGCATGCTAGCAAAAGAACTTTGAACCTGG	3300
QY	3301	ATCCAATTTATGCTGATGCTCAAGGCTTGAACCTTTGTTAGAGAACTTGGACATG	3360
DB	3301	ATCCAATTTATGCTGATGCTCAAGGCTTGAACCTTTGTTAGAGAACTTGGACATG	3360
QY	3361	CAATGGCCAAATTTGTTGAGCGTTTAAAGGAGCTTTTACTTTGGAGGAAAGCTTGGAGG	3420
DB	3361	CAATGGCCAAATTTGTTGAGCGTTTAAAGGAGCTTTTACTTTGGAGGAAAGCTTGGAGG	3420
QY	3421	AAGCCAAAGCAGTTATTTGGACGCTTGTCTTTTAAATGATCCGGACCTTGCAGAGTCTGGC	3480
DB	3421	AAGCCAAAGCAGTTATTTGGACGCTTGTCTTTTAAATGATCCGGACCTTGCAGAGTCTGGC	3480
QY	3481	TCAAATTTCTCTCCACCCACTTCCAACTCAAGAGCCAAATACATGATCGCAAACTTTATTTG	3540
DB	3481	TCAAATTTCTCTCCACCCACTTCCAACTCAAGAGCCAAATACATGATCGCAAACTTTATTTG	3540
QY	3541	AAACTTCTCCAGTTCTCAAAAACCTTACTGAGTTTGAAGAGCAATTTGAGTAATTTTAA	3600
DB	3541	AAACTTCTCCAGTTCTCAAAAACCTTACTGAGTTTGAAGAGCAATTTGAGTAATTTTAA	3600
QY	3601	CTCATGTTTCGACTTCTGCGCAAGGCAATTCACATTCAGAACTCTGGGATTTAAACCATCTGA	3660
DB	3601	CTCATGTTTCGACTTCTGCGCAAGGCAATTCACATTCAGAACTCTGGGATTTAAACCATCTGA	3660
QY	3661	CCCTAGGCCCAATCAGAGAAATGGAATTCCTAGGTGACTCCATAATGCAACTTGGTAGCCA	3720
DB	3661	CCCTAGGCCCAATCAGAGAAATGGAATTCCTAGGTGACTCCATAATGCAACTTGGTAGCCA	3720
QY	3721	CAGAGTACTTATTATTTCATTTCCAGATCATCATGAGGACACTTAACTTTGTTGCGAA	3780
DB	3721	CAGAGTACTTATTATTTCATTTCCAGATCATCATGAGGACACTTAACTTTGTTGCGAA	3780
QY	3781	GCTCTTTGTTGTAATTAATAGAACTCAGGCCAAGGTAGCGAGGAGCTGGGCATGCAAGAGT	3840
DB	3781	GCTCTTTGTTGTAATTAATAGAACTCAGGCCAAGGTAGCGAGGAGCTGGGCATGCAAGAGT	3840
QY	3841	AGGCCAATAACCAACGACCAAGAGCCCTGTGGCGCTTCGCAACCAAGACTTTGGCGG	3900
DB	3841	AGGCCAATAACCAACGACCAAGAGCCCTGTGGCGCTTCGCAACCAAGACTTTGGCGG	3900
QY	3901	ACCTTTTGGAAATCATTTTATTTGACGCGCTGTACATGATTAAGGATTTGGGAATATGTTTATA	3960

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3901 ACCTTTGGAACTATTATTCAGCGCTGACACTGATAAGGATTGGAAATATGTTGATA 3960
|||||
3961 CTTTCATGAATGTCTGCTCTTTCCACGATTAAGAAATTCATTTTGAATCAGGATTGGA 4020
|||||
3961 CTTTCATGAATGTCTGCTCTTTCCACGATTAAGAAATTCATTTTGAATCAGGATTGGA 4020
|||||
4021 ATGACCCCAAAATCCACAGCTTCAGCAGTGTGCTTGACACTTAGGACAGAAAGAGAGC 4080
|||||
4021 ATGACCCCAAAATCCACAGCTTCAGCAGTGTGCTTGACACTTAGGACAGAAAGAGAGC 4080
|||||
4081 CAGACATTCCTCTGTACAAAGACTCTTGACAGAGTGGGCCCATCCCATGCCGAACTTACA 4140
|||||
4081 CAGACATTCCTCTGTACAAAGACTCTTGACAGAGTGGGCCCATCCCATGCCGAACTTACA 4140
|||||
4141 CTGTGGCTGTTTATTTCAAGGAGAGAAAGAAATAGGCTGTGGGAAAGACCAAGTATTTCAGC 4200
|||||
4141 CTGTGGCTGTTTATTTCAAGGAGAGAAAGAAATAGGCTGTGGGAAAGACCAAGTATTTCAGC 4200
|||||
4201 AAGCGAAATGGGAGCAGCAATGGATGGCTTGGAAAAATATAATTTTCCCGAGATGGCCC 4260
|||||
4201 AAGCGAAATGGGAGCAGCAATGGATGGCTTGGAAAAATATAATTTTCCCGAGATGGCCC 4260
|||||
4261 ATCAGAAGCGGTTTCATCGAACGGAAGTACAGACAGAGTTAAAGAAATCAGGTGGGAAA 4320
|||||
4261 ATCAGAAGCGGTTTCATCGAACGGAAGTACAGACAGAGTTAAAGAAATCAGGTGGGAAA 4320
|||||
4321 GAGAGCATCAAGAGAGAGAGCCAGATGAGATCGAAGACATCAAGAAATTAAGAGAGGCGAT 4380
|||||
4321 GAGAGCATCAAGAGAGAGAGCCAGATGAGATCGAAGACATCAAGAAATTAAGAGAGGCGAT 4380
|||||
4381 GCAAGTGTGGAGTATTACTTCTCAGTAACGTGACTGTGCTATTGACACCTAGCCCT 4440
|||||
4381 GCAAGTGTGGAGTATTACTTCTCAGTAACGTGACTGTGCTATTGACACCTAGCCCT 4440
|||||
4441 AGTTTTCCTGCGACAAATGAACGAAGTGTGCTCAATTGAAATAAATACAGAGTCAAATCG 4500
|||||
4441 AGTTTTCCTGCGACAAATGAACGAAGTGTGCTCAATTGAAATAAATACAGAGTCAAATCG 4500
|||||
4501 CTATTGCTGTTTAAATGATCTGTTTTTAGCTGATGATGCTTTTATTAACAAGTATTAGATT 4560
|||||
4501 CTATTGCTGTTTAAATGATCTGTTTTTAGCTGATGATGCTTTTATTAACAAGTATTAGATT 4560
|||||
4561 TTTCTTCTATTAAACGGAACCTTGACTTTGGTGAATGTGCATTACTCTCTTTTATTG 4620
|||||
4561 TTTCTTCTATTAAACGGAACCTTGACTTTGGTGAATGTGCATTACTCTCTTTTATTG 4620
|||||
4621 CTCTTTAAATATAAAATTAAGAAGCATATTCTATGTGGAATAGATCCTGTTTTTCCAT 4680
|||||
4621 CTCTTTAAATATAAAATTAAGAAGCATATTCTATGTGGAATAGATCCTGTTTTTCCAT 4680
|||||
4681 CTGTGCCCAGATTGTGACCCCTAGACTTTCAATTTGACAAGTAAAAAATTGACTTTACTAG 4740
|||||
4681 CTGTGCCCAGATTGTGACCCCTAGACTTTCAATTTGACAAGTAAAAAATTGACTTTACTAG 4740
|||||
4741 TAAAAAATAAAAAATAAAAAATAAAAA 4764
|||||
4741 TAAAAAATAAAAAATAAAAAATAAAAA 4764

RESULT 8
ADY17385
ID ADY17385 standard; DNA; 4764 BP.
XX
AC
ADY17385;
XX
DT 05-MAY-2005 (first entry)
XX
DE DNA encoding a PRO polypeptide, SEQ ID NO 3191.
XX
KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
KW Antichyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;

KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
KW Antiallergic; ds; gene; diagnosis.
XX
OS Homo sapiens.
XX WO2005016962-A2.
XX
PD 24-FEB-2005.
XX
PF 11-AUG-2004; 2004WO-US026249.
XX
PR 11-AUG-2003; 2003US-0493546P.
XX (GETH) GENENTECH INC.
XX
PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
DR WPI; 2005-182330/19.
XX
PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
PS Claim 1; SEQ ID NO 3191; 158pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
CC polypeptide.
XX
SQ Sequence 4764 BP; 1379 A; 1138 C; 1082 G; 1165 T; 0 U; 0 Other;

Query Match 99.9%; Score 4760.8; DB 14; Length 4764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4762; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGTCTGTGCTACTCGGCTAGTAGCTGGCTTTGCTCTGACGGCGATCTCGGGGCCGAG 60
DB 1 CTGTCTGTGCTACTCGGCTAGTAGCTGGCTTTGCTCTGACGGCGATCTCGGGGCCGAG 60
QY 61 AGCCTTTTATATGTTGCTTTTCCCGGGGATGTAAGGATACAGAAATGACTGTGAATCAA 120
DB 61 AGCCTTTTATATGTTGCTTTTCCCGGGGATGTAAGGATACAGAAATGACTGTGAATCAA 120
QY 121 CCCATATCATCAAGAGCTGATAAATCTAGTGAAGAGTTAGACGTGTGCATACCTTCACTA 180
DB 121 CCCATATCATCAAGAGCTGATAAATCTAGTGAAGAGTTAGACGTGTGCATACCTTCACTA 180
QY 181 TGATATGAGGCGAGTCTCTGAGCTTATTTCTCTGTGGAAGATGTGACATATCCAGGCGGA 240
DB 181 TGATATGAGGCGAGTCTCTGAGCTTATTTCTCTGTGGAAGATGTGACATATCCAGGCGGA 240
QY 241 ACATCATGATGAGGGAACACATGTCACAGAAATGTCTTCCACCGGACGAGGCGTC 300
DB 241 ACATCATGATGAGGGAACACATGTCACAGAAATGTCTTCCACCGGACGAGGCGTC 300
QY 301 CCCGAGGACGAGGAGGACATGGAGCCAGACCTTCAGCACCATCTTTAGGCCCCCAAAATC 360
DB 301 CCCGAGGACGAGGAGGACATGGAGCCAGACCTTCAGCACCATCTTTAGGCCCCCAAAATC 360
QY 361 TGAGGCTGCTTCCACCTTCAGGAGCTTCTGTGCAATATCAATATGAACTTCCAAAGTGCCC 420
DB 361 TGAGGCTGCTTCCACCTTCAGGAGCTTCTGTGCAATATCAATATGAACTTCCAAAGTGCCC 420
QY 421 CTTTCCACCACTTTTCTCAAACTCTCCAGCCCCCAATTTTCTCCCTCCACGACGAGCTTTG 480
DB 421 CTTTCCACCACTTTTCTCAAACTCTCCAGCCCCCAATTTTCTCCCTCCACGACGAGCTTTG 480
QY 481 TACCTTCCCCCACCACCATGCTTCCGTGAGCGAGGCGCTCTTCCCGCTGCCCCCAATCA 540
DB 481 TACCTTCCCCCACCACCATGCTTCCGTGAGCGAGGCGCTCTTCCCGCTGCCCCCAATCA 540

QY	541	GGCGGCTTTTCCCAACCA	CCAGATGAGGCA	CCCCCTTCC	CAGTTCTCTGTTTTCCTC	600		
DB	541	GGCGGCTTTTCCCAACCA	CCAGATGAGGCA	CCCCCTTCC	CAGTTCTCTGTTTTCCTC	600		
QY	601	CCATGCCACCA	CAATGCCCTTGCTTA	TAACCCCCC	CAGTCCCTTGGGGCACCTCCTGGAC	660		
DB	601	CCATGCCACCA	CAATGCCCTTGCTTA	TAACCCCCC	CAGTCCCTTGGGGCACCTCCTGGAC	660		
QY	661	AAGGCACTTTCCCTT	CAATGATGCCCCCTCCT	CCATGCTCAT	GCCTCCGCGCCCCCTCCAG	720		
DB	661	AAGGCACTTTCCCTT	CAATGATGCCCCCTCCT	CCATGCTCAT	GCCTCCGCGCCCCCTCCAG	720		
QY	721	TCATSCGGAGAGGTT	TAATTAATCAGTAC	CCCTCGGGCTATTCT	CACCACAATCTCCAC	780		
DB	721	TCATSCGGAGAGGTT	TAATTAATCAGTAC	CCCTCGGGCTATTCT	CACCACAATCTCCAC	780		
QY	781	CTCCCACTTTTAAT	AGTTTCCAGAA	CAACCCCTAGTTCT	TCTTCCCTGCCCCAGTGCTAAATAACA	840		
DB	781	CTCCCACTTTTAAT	AGTTTCCAGAA	CAACCCCTAGTTCT	TCTTCCCTGCCCCAGTGCTAAATAACA	840		
QY	841	GCAGTAGTCTCTA	TTTCCAGACATCT	CCCTCCATAC	CCCACTCCCAAGGCTCCCAAGTGAGA	900		
DB	841	GCAGTAGTCTCTA	TTTCCAGACATCT	CCCTCCATAC	CCCACTCCCAAGGCTCCCAAGTGAGA	900		
QY	901	GAAGGTCCCCAGAA	AGGCTGAAACAT	ATATGATGAC	CAACAGGCA	CCGAGACCA	CAGTCATG	960
DB	901	GAAGGTCCCCAGAA	AGGCTGAAACAT	ATATGATGAC	CAACAGGCA	CCGAGACCA	CAGTCATG	960
QY	961	GGCGAGGTGAG	GGCATCGGTCT	CGATCGGGGAG	CGAGCGCGAGTCCCGACAGGA	1020		
DB	961	GGCGAGGTGAG	GGCATCGGTCT	CGATCGGGGAG	CGAGCGCGAGTCCCGACAGGA	1020		
QY	1021	GAAGACAAGA	CAGCCGGTAC	AGTATGATGAC	CCGAGGGAGAAC	CCATCTCGCCACC	1080	
DB	1021	GAAGACAAGA	CAGCCGGTAC	AGTATGATGAC	CCGAGGGAGAAC	CCATCTCGCCACC	1080	
QY	1081	CGAGCTACGAA	CGGAGAGCGAGAAC	CGGAGAGAC	ACAGGCA	TGAGACAA	CCGAA	1140
DB	1081	CGAGCTACGAA	CGGAGAGCGAGAAC	CGGAGAGAC	ACAGGCA	TGAGACAA	CCGAA	1140
QY	1141	GATCACCATCT	CTGGAAAGTCT	TACAAAAGAGTAT	AGAGATCT	CTGGAAAGGATTACG	1200	
DB	1141	GATCACCATCT	CTGGAAAGTCT	TACAAAAGAGTAT	AGAGATCT	CTGGAAAGGATTACG	1200	
QY	1201	GTTTATCGGTTG	TCTCGAACCTGCT	GGATGCA	CACAGAA	TTTACCTGGGGAGATTATTA	1260	
DB	1201	GTTTATCGGTTG	TCTCGAACCTGCT	GGATGCA	CACAGAA	TTTACCTGGGGAGATTATTA	1260	
QY	1261	AAATAACAGAT	TTCTGGGCCCCA	CCCCCTGGAGAT	TGTGAATCAT	CGTCCCCCAAGTAGGG	1320	
DB	1261	AAATAACAGAT	TTCTGGGCCCCA	CCCCCTGGAGAT	TGTGAATCAT	CGTCCCCCAAGTAGGG	1320	
QY	1321	AGNAGAGAGAG	CTCTGGGAGAGAA	AAAGACGTTGGAGT	GCACACCA	CGAGGTTCTG	1380	
DB	1321	AGNAGAGAGAG	CTCTGGGAGAGAA	AAAGACGTTGGAGT	GCACACCA	CGAGGTTCTG	1380	
QY	1381	GCAAGACAAGAA	CTATACCTCAAT	CAAGGAAAAG	AGCCCGAGGAGAC	CATCGCTGACA	1440	
DB	1381	GCAAGACAAGAA	CTATACCTCAAT	CAAGGAAAAG	AGCCCGAGGAGAC	CATCGCTGACA	1440	
QY	1441	AGAATCAGGAG	GGAAGAGAACTT	CTTAAGCCTG	TGTGGATT	CGATGCAC	TTTCAG	1500
DB	1441	AGAATCAGGAG	GGAAGAGAACTT	CTTAAGCCTG	TGTGGATT	CGATGCAC	TTTCAG	1500
QY	1501	AAAATCTACT	CTCAGTGACCC	CAATCGAT	CGGTGGAGAT	TTCTCAGTGGT	TGGAACGA	1560
DB	1501	AAAATCTACT	CTCAGTGACCC	CAATCGAT	CGGTGGAGAT	TTCTCAGTGGT	TGGAACGA	1560
QY	1561	GTAGGCTTCTG	ACTTATATGACAA	ATTTTGGAGGAGT	TGGGAGCAGG	CAAGAAAGG	1620	
DB	1561	GTAGGCTTCTG	ACTTATATGACAA	ATTTTGGAGGAGT	TGGGAGCAGG	CAAGAAAGG	1620	

QY	1621	CAAAAGCTCT	CGCCTCGTGGAA	ACCTCCAAAG	ACGAGCTCGAT	GAAGATTTAGAGA	1680		
DB	1621	CAAAAGCTCT	CGCCTCGTGGAA	ACCTCCAAAG	ACGAGCTCGAT	GAAGATTTAGAGA	1680		
QY	1681	GTTTCCAGTGA	ATCCGAGTGTGAGT	CTGATGAG	CACGACCTCTGTT	TAGCAGTCA	GACT	1740	
DB	1681	GTTTCCAGTGA	ATCCGAGTGTGAGT	CTGATGAG	CACGACCTCTGTT	TAGCAGTCA	GACT	1740	
QY	1741	CTGAAGTTTTG	AGCGTTATTCAGAA	ATCMAACG	CAAAAAGGCC	CCCTGACCG	CTTC	1800	
DB	1741	CTGAAGTTTTG	AGCGTTATTCAGAA	ATCMAACG	CAAAAAGGCC	CCCTGACCG	CTTC	1800	
QY	1801	ATGATCAACT	TTTGGTAAACGAT	TCCAGG	CCAGATGAAT	TGATGACCA	CTCTGCAAA	TGCA	1860
DB	1801	ATGATCAACT	TTTGGTAAACGAT	TCCAGG	CCAGATGAAT	TGATGACCA	CTCTGCAAA	TGCA	1860
QY	1861	GCCAAAGGCA	GACGACGACAGG	CAATTAGG	CAAGCATTTAT	CTCTGGAG	AAGAGGCC	CATCA	1920
DB	1861	GCCAAAGGCA	GACGACGACAGG	CAATTAGG	CAAGCATTTAT	CTCTGGAG	AAGAGGCC	CATCA	1920
QY	1921	AGCCCTGT	CGTCTATGACAA	CAATGCTGG	CGACACTTTT	TCCACTAC	CCGATCACAGTCT	1980	
DB	1921	AGCCCTGT	CGTCTATGACAA	CAATGCTGG	CGACACTTTT	TCCACTAC	CCGATCACAGTCT	1980	
QY	1981	CCCCGCTAC	GAACTTTTAA	CTGACAGG	CCAACTGTTAT	TAGATACG	ATGATCACAGT	2040	
DB	1981	CCCCGCTAC	GAACTTTTAA	CTGACAGG	CCAACTGTTAT	TAGATACG	ATGATCACAGT	2040	
QY	2041	ATATCTTTCA	AGGATTTCTAT	GTGTCAT	ATGCCCCCT	CGACCAAT	TATTTCCACT	GTGA	2100
DB	2041	ATATCTTTCA	AGGATTTCTAT	GTGTCAT	ATGCCCCCT	CGACCAAT	TATTTCCACT	GTGA	2100
QY	2101	AAGTAATTA	GATTTCAA	CATAGACTA	CA	CGATTCA	TTTCA	TTGAAGATGATCCCGGAGA	2160
DB	2101	AAGTAATTA	GATTTCAA	CATAGACTA	CA	CGATTCA	TTTCA	TTGAAGATGATCCCGGAGA	2160
QY	2161	ATTTTGTGTG	AAAGGGCTTGA	ACTCTTTT	CACTGTTCT	TATTCAGATAT	TTTTTGGAT	2220	
DB	2161	ATTTTGTGTG	AAAGGGCTTGA	ACTCTTTT	CACTGTTCT	TATTCAGATAT	TTTTTGGAT	2220	
QY	2221	TATATGACT	GGAATCTTAA	AGGTCTTT	GTGTAAGACAG	ACCCCTCGCT	CGCCCAAGAT	2280	
DB	2221	TATATGACT	GGAATCTTAA	AGGTCTTT	GTGTAAGACAG	ACCCCTCGCT	CGCCCAAGAT	2280	
QY	2281	TTCAATTCAT	GCCACGTTTT	TTGAAGATTT	CTTCCAGAT	CGAGAAAG	AGTGTCTGTCCA	2340	
DB	2281	TTCAATTCAT	GCCACGTTTT	TTGAAGATTT	CTTCCAGAT	CGAGAAAG	AGTGTCTGTCCA	2340	
QY	2341	TGCACCA	GATTTCTCTG	TACTTTG	TAAAGTGCAG	CAAGCCCTGGT	GCCTGAGGAGAGA	2400	
DB	2341	TGCACCA	GATTTCTCTG	TACTTTG	TAAAGTGCAG	CAAGCCCTGGT	GCCTGAGGAGAGA	2400	
QY	2401	TTGGCCAAT	TATGCTTCA	GTCGGAGAG	CTGAGTGG	CGAGAAATAT	CAGAAAGATGCAAG	2460	
DB	2401	TTGGCCAAT	TATGCTTCA	GTCGGAGAG	CTGAGTGG	CGAGAAATAT	CAGAAAGATGCAAG	2460	
QY	2461	GCATGATTT	GTATACCA	ACCCCTGGG	ACGAAACCA	AGCTCTG	TCGATCGATCA	CTGGATC	2520
DB	2461	GCATGATTT	GTATACCA	ACCCCTGGG	ACGAAACCA	AGCTCTG	TCGATCGATCA	CTGGATC	2520
QY	2521	GTGAACAG	TTTCAAC	CCCCCGATG	TAATCTTT	TCCGATTA	TCGTCCCA	CTTTGGGATACGCC	2580
DB	2521	GTGAACAG	TTTCAAC	CCCCCGATG	TAATCTTT	TCCGATTA	TCGTCCCA	CTTTGGGATACGCC	2580
QY	2581	CTGCA	CAGTTGATG	TATG	CAGGAGCC	CACAGTAC	CAAAACT	TGTCGAAAGATTATGTGA	2640
DB	2581	CTGCA	CAGTTGATG	TATG	CAGGAGCC	CACAGTAC	CAAAACT	TGTCGAAAGATTATGTGA	2640
QY	2641	AACTTCG	CACTCTCT	TAGCAAA	TAGTCC	CAAAAGT	CAAACTGA	CAAAACAGAACTGG	2700
DB	2641	AACTTCG	CACTCTCT	TAGCAAA	TAGTCC	CAAAAGT	CAAACTGA	CAAAACAGAACTGG	2700
QY	2701	CACAGAGG	GGAAGGCC	CTTCCAAA	AAATATAC	GGCAGAA	GAATATCA	ATGAGACGAGAAAGTAA	2760

Db	2701	 CACAGAGGAGGAGGCCCTCCAAAAATACGGCAGAGAAATACAATGAGACGAGAAGTAA	2760
Qy	2761	CGGTGGAGCTAAGTATAGCAAGGATTCGGAAACTCGGCATCCGTTCTGTATGTCGTGTCAGC	2820
Db	2761	CGGTGGAGCTAAGTATAGCAAGGATTCGGAAACTCGGCATCCGTTCTGTATGTCGTGTCAGC	2820
Qy	2821	ATGCAATGATGCTACCTGTTCGACCCATCATATCCGCTACCAACCAATGCTTAATGCATT	2880
Db	2821	ATGCAATGATGCTACCTGTTCGACCCATCATATCCGCTACCAACCAATGCTTAATGCATT	2880
Qy	2881	TGGCAAAAGTTGATAGGATATATCTTCCAAAGATCGTTGCTGTGGAGCTGGCCATGACTC	2940
Db	2881	TGGCAAAAGTTGATAGGATATATCTTCCAAAGATCGTTGCTGTGGAGCTGGCCATGACTC	2940
Qy	2941	ATCCAGTGCATCATTTAAATTTTGGATGAATCCTGATCATGCGCAGGAATTCATTAATCTA	3000
Db	2941	ATCCAGTGCATCATTTAAATTTTGGATGAATCCTGATCATGCGCAGGAATTCATTAATCTA	3000
Qy	3001	ACTGTGGAAATTCGGCAGCCCCAAATACCGGAGACAGAAAGTTTCATCATGCACATGCGGA	3060
Db	3001	ACTGTGGAAATTCGGCAGCCCCAAATACCGGAGACAGAAAGTTTCATCATGCACATGCGGA	3060
Qy	3061	AGAAAGGGAATTAACACTTGTGATAAATATCATGTCAOGCCTTGGCCAAAGATGACCCAACTC	3120
Db	3061	AGAAAGGGAATTAACACTTGTGATAAATATCATGTCAOGCCTTGGCCAAAGATGACCCAACTC	3120
Qy	3121	CCTCGAGGATTAACCAACAATGAACGGTTGGAAATTCCTGGGTGATGCTGTGTTGGAATTTTC	3180
Db	3121	CCTCGAGGATTAACCAACAATGAACGGTTGGAAATTCCTGGGTGATGCTGTGTTGGAATTTTC	3180
Qy	3181	TGACCAAGCTCCATTTCGTACTATTGTTTCTCTAGTCTGGAAGAGGAGGATTAAGCAACCT	3240
Db	3181	TGACCAAGCTCCATTTCGTACTATTGTTTCTCTAGTCTGGAAGAGGAGGATTAAGCAACCT	3240
Qy	3241	ATCGGACTGGCAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTGGAGGGAAGCCTGGAGG	3300
Db	3241	ATCGGACTGGCAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTGGAGGGAAGCCTGGAGG	3300
Qy	3301	ATCCATTATGCTGTATGCTCAGCGGCGCTGACCTTTGTAGAGATCGGACCTTCGCATG	3360
Db	3301	ATCCATTATGCTGTATGCTCAGCGGCGCTGACCTTTGTAGAGATCGGACCTTCGCATG	3360
Qy	3361	CAATGGCCAAATGTTTGAAGCGTTAATAGGAGCTGTTTACTTGGAGGGAAGCCTGGAGG	3420
Db	3361	CAATGGCCAAATGTTTGAAGCGTTAATAGGAGCTGTTTACTTGGAGGGAAGCCTGGAGG	3420
Qy	3421	AAGCCAAAGCAGTTAATTTGGAACGTTGCTCTTTAATGATCCGGACCTCGCGAAGCTTGGC	3480
Db	3421	AAGCCAAAGCAGTTAATTTGGAACGTTGCTCTTTAATGATCCGGACCTCGCGAAGCTTGGC	3480
Qy	3481	TCAATTATCTCTCCACCCACTCAACTACAGAGCCAAATACATGATCGGCAACTTATTG	3540
Db	3481	TCAATTATCTCTCCACCCACTCAACTACAGAGCCAAATACATGATCGGCAACTTATTG	3540
Qy	3541	AAACCTCTCCAGTTCTACAAAACCTTACTGAGTTTGAAGAGCAATTTGGAGTAAATTTTA	3600
Db	3541	AAACCTCTCCAGTTCTACAAAACCTTACTGAGTTTGAAGAGCAATTTGGAGTAAATTTTA	3600
Qy	3601	CTCATGTTTGCATTTCTGGCAAGGCCATTCATTCATGAGAACTGTGGGATTTAAACCATCTGA	3660
Db	3601	CTCATGTTTGCATTTCTGGCAAGGCCATTCATTCATGAGAACTGTGGGATTTAAACCATCTGA	3660
Qy	3661	CCCTAGGCCCAAACTCAGAGAAATGGAATTCCTTAGTGACTCCATTAATGCCAACTGGTAGCCA	3720
Db	3661	CCCTAGGCCCAAACTCAGAGAAATGGAATTCCTTAGTGACTCCATTAATGCCAACTGGTAGCCA	3720
Qy	3721	CAGAGTACTTATTCATTCTTTCCAGATCATCATGAGGACCTTAACCTTTGTTGGCAA	3780
Db	3721	CAGAGTACTTATTCATTCTTTCCAGATCATCATGAGGACCTTAACCTTTGTTGGCAA	3780
Qy	3781	GCTCTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGGCATGCGAGGT	3840

Db	3781	GCTCTTTGGTGAATATATAGAACTTCAGGCCAAGGTAGCGGAGGAGCTGGCGCATCCAGGAGT	3841
Qy	3841	ACGCCATAACCAACGACCAAGACCAAGAGGCGCTGTGGCGCTTCGCACCAAGACCTTTGCGCG	3901
Db	3841	ACGCCATAACCAACGACCAAGACCAAGAGGCGCTGTGGCGCTTCGCACCAAGACCTTTGCGCG	3901
Qy	3901	ACCTTTTGGAAATCATTTATTGAGCGCGTGTACTCATTAAGGATTTTGGATATGTTTCATA	3961
Db	3901	ACCTTTTGGAAATCATTTATTGACAGCGCTGTACTCATTAAGGATTTTGGATATGTTTCATA	3961
Qy	3961	CTTTTCATGAATGTCGTCTCTTTTCCACGATTGAAAGAAATTCATTTTGGAAATCAGGATTTGGA	4021
Db	3961	CTTTTCATGAATGTCGTCTCTTTTCCACGATTGAAAGAAATTCATTTTGGAAATCAGGATTTGGA	4021
Qy	4021	ATGACCCCAAAATCCCAGCTTTCAGCAGTGTGCTTGTGACACTTAGGACAGAGGAAAAAGAGC	4081
Db	4021	ATGACCCCAAAATCCCAGCTTTCAGCAGTGTGCTTGTGACACTTAGGACAGAGGAAAAAGAGC	4081
Qy	4081	CAGACATTCCTCTGTGTACAGACTCTGCGACAGCTGGGGCCCATCCCATGCCGCAACCTTACA	4141
Db	4081	CAGACATTCCTCTGTGTACAGACTCTGCGACAGCTGGGGCCCATCCCATGCCGCAACCTTACA	4141
Qy	4141	CTGTGGCTGTTTATTTTCAAGGGAGAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTTCAGC	4201
Db	4141	CTGTGGCTGTTTATTTTCAAGGGAGAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTTCAGC	4201
Qy	4201	AAGCGGAAATGGGAGCAGCAATCGATTCGCTTGAAAAATATAATTTTCCCAGATGGCCC	4261
Db	4201	AAGCGGAAATGGGAGCAGCAATCGATTCGCTTGAAAAATATAATTTTCCCAGATGGCCC	4261
Qy	4261	ATCAGAAAGCGGTTTCATCGAACGGAATGTACAGACAGAGTTTAAAGAAATGAGGTGGGAAA	4321
Db	4261	ATCAGAAAGCGGTTTCATCGAACGGAATGTACAGACAGAGTTTAAAGAAATGAGGTGGGAAA	4321
Qy	4321	GAGAGCATCAAGAGAGAGAGCCAGATGTAGACTGAAGACATCAAGAAATAAAGGAGGGCAT	4381
Db	4321	GAGAGCATCAAGAGAGAGAGCCAGATGTAGACTGAAGACATCAAGAAATAAAGGAGGGCAT	4381
Qy	4381	GCAAGTGTGGAGTATTTACTTGTCTCAGTAACTGTGACTGTGTGCTATTTAGAGACTAGCCT	4441
Db	4381	GCAAGTGTGGAGTATTTACTTGTCTCAGTAACTGTGACTGTGTGCTATTTAGAGACTAGCCT	4441
Qy	4441	AGTTTTCTTCGACACAAATGAACCAAGTGTCTCATTTGAAATAAAATACAGAGTCAAAATCG	4501
Db	4441	AGTTTTCTTCGACACAAATGAACCAAGTGTCTCATTTGAAATAAAATACAGAGTCAAAATCG	4501
Qy	4501	CTATTGTTGTTTAAATGATCTGTTTTTAGCTGGATGGTCTTTATTATCAAAAGTATTAGATT	4561
Db	4501	CTATTGTTGTTTAAATGATCTGTTTTTAGCTGGATGGTCTTTATTATCAAAAGTATTAGATT	4561
Qy	4561	TTTTCTTCTATTAAACGGAACCTTGACTTTTGGTGAATGTGCATTTACTTCCTTTTATTTTG	4621
Db	4561	TTTTCTTCTATTAAACGGAACCTTGACTTTTGGTGAATGTGCATTTACTTCCTTTTATTTTG	4621
Qy	4621	CTCTTTAAATAATAAAATTCAGAGACATATCTTATGTGGAATAGATCTCTGTTTTTCCAT	4681
Db	4621	CTCTTTAAATAATAAAATTCAGAGACATATCTTATGTGGAATAGATCTCTGTTTTTCCAT	4681
Qy	4681	CTGTGTCCCAGATTGTGACCCCTAGACTTTTCAATTGTGACCAAGTAAAAAATTTGACTTTACTAG	4741
Db	4681	CTGTGTCCCAGATTGTGACCCCTAGACTTTTCAATTGTGACCAAGTAAAAAATTTGACTTTACTAG	4741
Qy	4741	TAAAAAATAAAAAAAAAAAAAAAAAAAAAA 4764	
Db	4741	TAAAAAATAAAAAAAAAAAAAAAAAAAAAA 4764	

RESULT 9
ADQ22183
ID ADQ22183 standard; DNA; 5425 BP.
XX
XX ADQ22183;
XX

DT 26-AUG-2004 (first entry)
XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 5003.
DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW db.
XX Homo sapiens.
OS
XX WO2004048938-A2.
PN 10-JUN-2004.
XX
XX 26-NOV-2003; 2003WO-US038193.
PF 26-NOV-2002; 2002US-0429739P.
XX (PROT-) PROTEIN DESIGN LABS INC.
PR
XX Aziz N, Ginsburg WM, Zlotnik A;
PI WPI; 2004-441208/41.
XX
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
XX Example 2; SEQ ID NO 5003; 210pp; English.
PS
XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytotatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 5425 BP; 1583 A; 1257 C; 1234 G; 1349 T; 0 U; 2 Other;
Query Match 99.3%; Score 4732.4; DB 12; Length 5425;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4751; Conservative 0; Mismatches 11; Indels 2; Gaps 1;
QY 1 CTGTCTTGTTAGTCTGCGGTAGTACCTGGCTTTGCTCTGACGCGGATCTCGCGGCCCGAG 60
DB 101 CTGTCTTGTTAGTCTGCGGTAGTACCTGGCTTTGCTCTGACGCGGATCTCGCGGCCCGAG 160
QY 61 AGCCTTTTATAGTCTGCTTTCCCGGGGATGGAAGGATACGAATGATGTGAATCAA 120
DB 161 AGCCTTTTATAGTCTGCTTTCCCGGGGATGGAAGGATACGAATGATGTGAATCAA 220
QY 121 CCATATCATCAAGGAGCTGATAATCTAGTGAAGAGTTAGAGCTGTGCATCTTCACTA 180
DB 221 CCATATCATCAAGGAGCTGATAATCTAGTGAAGAGTTAGAGCTGTGCATCTTCACTA 280
QY 181 TGATATGAGGCGAGTCTCTGAGCTTATATTTCTGTGGAAGAGTTAGAGCTGTGCATCTTCACTA 240
DB 281 TGATATGAGGCGAGTCTCTGAGCTTATATTTCTGTGGAAGAGTTAGAGCTGTGCATCTTCACTA 340
QY 241 ACATCATGATGAGGGAACACATGTCAAGAAATGTGTTCCACCCGGGACGAGGCGGTC 300
DB 341 ACATCATGATGAGGGAACACATGTCAAGAAATGTGTTCCACCCGGGACGAGGCGGTC 400
QY 301 CCGGAGGACGAGGAGACATGGAGCCAGACCTTCAGCACATCTTTAGGCCCCCAATC 360
DB 401 CCGGAGGACGAGGAGACATGGAGCCAGACCTTCAGCACATCTTTAGGCCCCCAATC 460

1441 AGAATGAGGAGGAAGAAGAACTCTTTAAAGCCTGTGTGGATTGATGCATCTCATTTAC 1500
1541 AGAATGAGGAGGAAGAAGAACTCTTTAAAGCCTGTGTGGATTGATGCATCTCATTTAC 1600
1501 AAAAATACTATCTCCAGTGAACCCCATGGATCAGGTGGGAGATTCTACAGTGGTTGGAAAGA 1560
1601 AAAAATACTATCTCCAGTGAACCCCATGGATCAGGTGGGAGATTCTACAGTGGTTGGAAAGA 1660
1561 GTAGGCTTCGTGACTTATATGACAAATTTGAGGAGGATTGGGAGCAGGCAAGAAAGG 1620
1661 GTAGGCTTCGTGACTTATATGACAAATTTGAGGAGGATTGGGAGCAGGCAAGAAAGG 1720
1621 CCAAGCTCTCGGCCCTCGTGGGAACCTCCAAAGACGAAGCTCGATGAAGATTATAGAGA 1680
1721 CCAAGCTCTCGGCCCTCGTGGGAACCTCCAAAGACGAAGCTCGATGAAGATTATAGAGA 1780
1681 GTTCCAGTGAATCCGAGTGTGATGTGATGAGGACAGCACCTGTTCTAGCAGCTCAGACT 1740
1781 GTTCCAGTGAATCCGAGTGTGATGTGATGAGGACAGCACCTGTTCTAGCAGCTCAGACT 1840
1741 CTGAAGTTTGTGACGTTATTCAGAAATCAAACGGCAAAAAGGCCACCTGACCGACTTC 1800
1841 CTGAAGTTTGTGACGTTATTCAGAAATCAAACGGCAAAAAGGCCACCTGACCGACTTC 1900
1801 ATGATCAACTTTGGTACAAAGATCCAGGCGCAGATGAATGATGACCACTCTGCMAATGCA 1860
1901 A--AGGAACCTTTGGTACAAAGATCCAGGCGCAGATGAATGATGACCACTCTGCMAATGCA 1958
1861 GGCMAAGGCAAGCAGCAGCAAGGAATTTAGGCACAGCATTTTATCCTGGAGGAAGGCCATCA 1920
1959 GGCMAAGGCAAGCAGCAGCAAGGAATTTAGGCACAGCATTTTATCCTGGAGGAAGGCCATCA 2018
1921 AGCCCTGTGCTGTATGACCAACATGCTGGCAGACTTTTCCACTACCGGATCAAGTCT 1980
2019 AGCCCTGTGCTGTATGACCAACATGCTGGCAGACTTTTCCACTACCGGATCAAGTCT 2078
1981 CCCGCGCTACGAACCTTTTAACTGACAGCGCAACTGTTATAGAAATACGATGATCAGAGT 2040
2079 CCCGCGCTACGAACCTTTTAACTGACAGCGCAACTGTTATAGAAATACGATGATCAGAGT 2138
2041 ATATCTTTGAAGGATTTCTATGTTTGCATATGCCCCCTCGACCAATATTCACATGTGTA 2100
2139 ATATCTTTGAAGGATTTCTATGTTTGCATATGCCCCCTCGACCAATATTCACATGTGTA 2198
2101 AGATAATAGATTCACATAGACTACACGATTCATTTCAATTGAGAGATGATGCGGAGA 2160
2199 AAGTAATAGATTCACATAGACTACACGATTCATTTCAATTGAGAGATGATGCGGAGA 2258
2161 ATTTTGTGTGAAGGGCTTGAACCTCTTTTCACTGTTCTTATTCAGAGATATTTTGGAAAT 2220
2259 ATTTTGTGTGAAGGGCTTGAACCTCTTTTCACTGTTCTTATTCAGAGATATTTTGGAAAT 2318
2221 TATATGACTGGAAATCTTAAAGGTCCTTGTGTTGAAGACAGCCCTCCCTGCTGCCAAGAT 2280
2319 TATATGACTGGAAATCTTAAAGGTCCTTGTGTTGAAGACAGCCCTCCCTGCTGCCAAGAT 2378
2281 TTCATTTTCATGCCACGTTTTGTGAAGATTTCTTCAGATGAGGAAGAGATGCTGTCCA 2340
2379 TTCATTTTCATGCCACGTTTTGTGAAGATTTCTTCCAGATGAGGAAGAGATGCTGTCCA 2438
2341 TGCAACAGATTTCTTCGTGTAACCTGTTAAGGTGACAGCAAGCCCTGGTGCCTGAGGAGAGA 2400
2439 TGCAACAGATTTCTTCGTGTAACCTGTTAAGGTGACAGCAAGCCCTGGTGCCTGAGGAGAGA 2498
2401 TTGCCAATATGCTTCAGTGGGAGAGCTGAGGTGGCAGAAATATGAGGAAGAAATGCAAAAG 2460
2499 TTGCCAATATGCTTCAGTGGGAGAGCTGAGGTGGCAGAAATATGAGGAAGAAATGCAAAAG 2558
2461 GCATGATTTGTATACCAACCCCTGGGACGAACCAAGCTCTGTCCGTATCGATCAACTGGATC 2520
2559 GCATGATTTGTATACCAACCCCTGGGACGAACCAAGCTCTGTCCGTATCGATCAACTGGATC 2618
2521 GTGAACAGTTTCAACCCCGATGTGATTTACTTTTCCGATTTATCGTCCACTTTTGGGATACGCC 2580

2619 GTGAACAGTTTCAACCCCGATGTGATTTACTTTTCCGATTTATCGTCCACTTTGGGATACGCC 2678
2581 CTGCAAGTTGAGTTTATCGAGGAGACCCACAGTACCAAAAACCTGTGGAAAGAGTTATGTGA 2640
2679 CTGCAAGTTGAGTTTATCGAGGAGACCCACAGTACCAAAAACCTGTGGAAAGAGTTATGTGA 2738
2641 AACTTTCGCCACCTCTAGCAAAATAGTCCCAAAGTCAAAACAACTGACAAACAGAAAGCTGG 2700
2739 AACTTTCGCCACCTCTAGCAAAATAGTCCCAAAGTCAAAACAACTGACAAACAGAAAGCTGG 2798
2701 CACAGAGGAGAAAGCCCTTCAAAAATAACGCGAGAAGATAAATCAATGAGAGACGAGAAGTAA 2760
2799 CACAGAGGAGAAAGCCCTTCAAAAATAACGCGAGAAGATAAATCAATGAGAGACGAGAAGTAA 2858
2761 CGGTGGAGCTAAGTAGTACCAAGGATTTCTGGAAACCTGGCATCCGTTCTGATGCTCTGCAGC 2820
2859 CGGTGGAGCTAAGTAGTACCAAGGATTTCTGGAAACCTGGCATCCGTTCTGATGCTCTGCAGC 2918
2821 ATGCAATGATGCTACTGTTCTGACCCCATCATATCCGCTTACCACCAATGCCCTAAATGCAAT 2880
2919 ATGCAATGATGCTACTGTTCTGACCCCATCATATCCGCTTACCACCAATGCCCTAAATGCAAT 2978
2881 TGGACAAGTTGATAGGATATATCTTTCCAAGATCGTTGTCTGTTGCAAGCTGGCCATGACTC 2940
2979 TGGACAAGTTGATAGGATATATCTTTCCAAGATCGTTGTCTGTTGCAAGCTGGCCATGACTC 3038
2941 ATCCAAGTCAATTTAAATTTTGGAAATGAAATCTCGATCATCCAGGAATTCATTTATCTTA 3000
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3061 AGAAAGGATTAACACCTTGTGATAAATATCATGTCAAGCTTGGCCCAAGATGACCCAACTC 3120
3159 AGAAAGGATTAACACCTTGTGATAAATATCATGTCAAGCTTGGCCCAAGATGACCCAACTC 3218
3121 CCTCGAGGATTAACACATGAAACGTTGGAAATCTCGGTGATGCTGTTGTGAAATTTTC 3180
3219 CCTCGAGGATTAACACATGAAACGTTGGAAATCTCGGTGATGCTGTTGTGAAATTTTC 3278
3181 TGACCAAGCTCATTTGTGATAAATATCTTTTCTAGTCTGGAAGAGAGGATTTAGCAACT 3240
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3241 ATCGGACTGCCATTTGTGAGAAATCAGCACTTTGCCATGCTAGCAAAAGAACTTTGAACCTGG 3300
3339 ATCGGACTGCCATTTGTGAGAAATCAGCACTTTGCCATGCTAGCAAAAGAACTTTGAACCTGG 3398
3301 ATCGAATTTATGCTGATGCTCAGCGGCTGACCTTTGTAGAGAAATCGGACCTTCGACATG 3360
3399 ATCGAATTTATGCTGATGCTCAGCGGCTGACCTTTGTAGAGAAATCGGACCTTCGACATG 3458
3361 CAATGCGCAATTTGTTTGAAGCGTTAAATAGGAGCTGTTTACTTTGAGGGAAGCTTGGAGG 3420
3459 CAATGCGCAATTTGTTTGAAGCGTTAAATAGGAGCTGTTTACTTTGAGGGAAGCTTGGAGG 3518
3421 AAGCCAAAGCAGTTATTTGGACGCTTGTCTTTTAAATGATCCGGAACCTTGCAGAGTCTGGC 3480
3519 AAGCCAAAGCAGTTATTTGGACGCTTGTCTTTTAAATGATCCGGAACCTTGCAGAGTCTGGC 3578
3481 TCAATTTATCTCTCCACCCACTCCAACTACAGAGCCAAATCTGATCCGCAACTTTATTG 3540
3579 TCAATTTATCTCTCCACCCACTCCAACTACAGAGCCAAATCTGATCCGCAACTTTATTG 3638
3541 AAACCTTCTCCAGTTCTACAAAAAATTTACTGAGTTTGAAGAGCAATTTGAGTAATTTTAA 3600
3639 AAACCTTCTCCAGTTCTACAAAAAATTTACTGAGTTTGAAGAGCAATTTGAGTAATTTTAA 3698
3601 CTCATGTTTCGACTTCTGGCAAGGCAATTCATTTGAGAACTGTGGGATTTAACCATCTGA 3660

3699 CTGATGTTGAGCTTCTGGCAAGGCGATTCACATTTGAGAACTGTGGGATTTAAACCATCTGA 3758
3661 CCTAGGCCACATCAGAGATGGAATCTTAGTGACTCTCAATAATGCAACTGGTAGCCA 3720
3759 CCTAGGCCACATCAGAGATGGAATCTTAGTGACTCTCAATAATGCAACTGGTAGCCA 3818
3721 CAGAGTACTTATTCAATTCATTTCCAGATCATCATGAAGGACACTTAACTTTGTCGGA 3780
3819 CAGAGTACTTATTCAATTCATTTCCAGATCATCATGAAGGACACTTAACTTTGTCGGA 3878
3781 GCTCTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGAGCTGGGCATGACAGAGT 3840
3879 GCTCTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGAGCTGGGCATGACAGAGT 3938
3841 AGCCCAATACCAACGACAGCAAGAGGCTGTGGCGCTTCGCAACAGACCTTGGCGG 3900
3939 AGCCCAATACCAACGACAGCAAGAGGCTGTGGCGCTTCGCAACAGACCTTGGCGG 3998
3901 ACCTTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGAGCTGGGCATGACAGAGT 3960
3999 ACCTTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGAGCTGGGCATGACAGAGT 4058
3961 CTTTCATGAATGTCCTCTTTCCACGATTTGAAGAATTCATTTTGAATCAGGATTTGA 4020
4059 CTTTCATGAATGTCCTCTTTCCACGATTTGAAGAATTCATTTTGAATCAGGATTTGA 4118
4021 ATGACCCCAATCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCT 4080
4119 ATGACCCCAATCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCT 4178
4081 CAGACATTCCTCTGTACAGACTCTCAGACAGTGGGCGCCATCCATGCGCCGACCTTCA 4140
4179 CAGACATTCCTCTGTACAGACTCTCAGACAGTGGGCGCCATCCATGCGCCGACCTTCA 4238
4141 CTGTGCTCTTTATTTCAAGGAGAGAAAGTATAGCTGTGGGAAAGGACCAAGTATTCAGC 4200
4239 CTGTGCTCTTTATTTCAAGGAGAGAAAGTATAGCTGTGGGAAAGGACCAAGTATTCAGC 4298
4201 AGCGGAATGGGAGAGCAATGGATGCGCTTGAAAAATATATTTTCCCGAGATGGCC 4260
4299 AGCGGAATGGGAGAGCAATGGATGCGCTTGAAAAATATATATTTTCCCGAGATGGCC 4358
4261 ATCAGAGCGGTTTCATCGAACGAGTACAGCAAGAGTTAAAGAAATGAGGTGGGAA 4320
4359 ATCAGAGCGGTTTCATCGAACGAGTACAGCAAGAGTTAAAGAAATGAGGTGGGAA 4418
4321 GAGAGCATCAAGAGAGAGCCAGATGAGACTCAAGACATCAAGAAATAAAGAGGGCAT 4380
4419 GAGAGCATCAAGAGAGAGCCAGATGAGACTCAAGACATCAAGAAATAAAGAGGGCAT 4478
4381 GCAAGTGTGGAGTATTTATCTGCTCAGTAACTGTGACTGTGCTATTCAGACCTTAGCT 4440
4479 GCAAGTGTGGAGTATTTATCTGCTCAGTAACTGTGACTGTGCTATTCAGACCTTAGCT 4538
4441 AGTTTCTCTCAGACATCAAGAGTGGCTCATTTGAATAAATACAGAGTCAATCG 4500
4539 AGTTTCTCTCAGACATCAAGAGTGGCTCATTTGAATAAATACAGAGTCAATCG 4598
4501 CTATTGTTCTTTAATGATCTGTTTTAGCTGGATGCTCTTTATTAACAAGTATTAGATT 4560
4599 CTATTGTTCTTTAATGATCTGTTTTAGCTGGATGCTCTTTATTAACAAGTATTAGATT 4658
4561 TTTCTTTCTAATAACGAAAACTTGAATTTGGTGAATGCAATCTCTTTTATTTTGG 4620
4659 TTTCTTTCTAATAACGAAAACTTGAATTTGGTGAATGCAATCTCTTTTATTTTGG 4718
4621 CTCCTTAATAATAAATTCAGAGCATTTCTATGTCGATAGATCTCTGTTTTCAT 4680
4719 CTCCTTAATAATAAATTCAGAGCATTTCTATGTCGATAGATCTCTGTTTTCAT 4778
4681 CTGTGTCAGAGTGTGACCTTAGACTTTCAATTTGACAGTAAAAAATGACTTTACTAG 4740
4779 CTGTGTCAGAGTGTGACCTTAGACTTTCAATTTGACAGTAAAAAATGACTTTACTAG 4838

QY 4741 TAAAAAATAAAAAAAAAAAAAA 4764
Db 4839 TAAAAAATAAAAAAAAAAAAAA 4862

RESULT 10

AE19628
ID AE19628 standard; cDNA; 3603 BP.
XX
AC AE19628;
XX
DT 11-AUG-2005 (first entry)
XX
DE Novel human polynucleotide SEQ ID NO 322.

XX
KW vulnary; CNS-gen.; gene therapy; diagnostic; forensic; mapping;
DNA purification; protein purification; osteoarthritis; antiarthritic;
osteopathic; musculoskeletal disease; osteoporosis; endocrine disease;
periodontal disease; antiinflammatory; mouth disease; burns; injury;
peripheral neuropathy; Alzheimers disease; neuroprotective; neurotropic;
degeneration; parkinsons disease; antiparkinsonian; neurological disease;
cerebrovascular ischemia; cerebroprotective; vasotropic;
cardiovascular disease; autoimmune disease; immunosuppressive;
immune disorder; viral infection; virucide; infection; cancer;
cytostatic; neoplasm; gene; ss.

XX Homo sapiens.

OS WO2005049806-A2.

PN 02-JUN-2005.

PD 11-MAR-2004; 2004WO-US007412.

PF 14-MAR-2003; 2003US-00389559.

PR (NUVE-) NUVELO INC.

XX Tang TY, Wang J, Wang ZW, Zhang J, Ren F, Zhou P, Ma Y;
PI Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;
PI Wehrman T, Weng G, Boyle B;

XX WPI; 2005-417730/42.
DR P-PSDB; AEA20195.

XX New polynucleotide encoding a polypeptide with biological activity,
PT useful for treating a disease or disorder, e.g. osteoarthritis, burns,
PT CNS and peripheral disease, stroke, autoimmune disorders, viral
PT infection, or cancer.

XX Claim 1; SEQ ID NO 322; 500pp; English.

XX The invention describes a new isolated polynucleotide (I) encoding a
CC polypeptide with biological activity comprising: a nucleotide sequence of
CC SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes
CC to the sequence of (I) under stringent hybridization conditions; or a
CC nucleotide sequence having greater than 99% sequence identity with the
CC sequence of (I). Also described are: a(n) (expression) vector comprising
CC (I); a host cell genetically engineered to comprise (I) operatively
CC associated with a regulatory sequence that modulates expression of the
CC polynucleotide in the host cell; an isolated polypeptide comprising a
CC sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide
CC is: a polypeptide encoded by (I); or a polypeptide encoded by a
CC polynucleotide hybridizing under stringent conditions with any one of SEQ
CC ID NOS: 1-567; a composition comprising the polypeptide of (3) and a
CC carrier; an antibody directed against the polypeptide of (3); a method
CC for detecting (I) in a sample; a method for detecting the polypeptide of
CC (3) in a sample; a method for identifying a compound that binds to the
CC polypeptide of (3); a method of producing the polypeptide of (3); and a
CC collection of polynucleotides, where the collection comprising of at
CC least one of SEQ ID NOS: 1-567. (I) is a polynucleotide comprising any of
CC the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological

activity, which comprises any of the amino acid sequence of SEQ ID NOS: 568-1134. All sequences are fully defined in the specification. The sequences and methods are useful in diagnostics, forensic, and gene mapping, in identifying of mutations responsible for genetic disorders or other traits, in assessing biodiversity, and for producing many other types of data and products dependent on DNA and amino acid sequences. The composition and method are useful for treating a disease or disorder, e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and peripheral disease, Alzheimer's disease, Parkinson's disease, stroke, autoimmune disorders, viral infection, or cancer. This sequence encodes a novel polypeptide of the invention.

Sequence 3603 BP; 1051 A; 860 C; 840 G; 852 T; 0 U; 0 Other;

Query Match	70.9%;	Score 3376.2;	DB 14;	Length 3603;
Best Local Similarity	94.4%;	Pred. No. 0;		
Matches 3595;	Conservative	0;	Mismatches 8;	Indels 204; Gaps 1;

QY	564	ATGAGGCACCCCTTCCCGAGTTCTCTCTGTGTTTCTCCATGCGCACACCAATGCGCTTGT	623
Db	1	ATGAGGCACCCCTTCCCGAGTTCTCTCTGTGTTTCTCCATGCGCACACCAATGCGCTTGT	60
QY	624	CCTAATAACCCGCCAGTCCCTGGGGCACCTCTGGACAAGGCATTTCCCTTTCATGATG	683
Db	61	CCTAATAACCCGCCAGTCCCTGGGGCACCTCTGGACAAGGCATTTTCCCTTTCATGATG	120
QY	684	CCCCCTCCCTCCATGCTCATCTCCCGCGCCCTCCAGTCATGTCGCGACAGGTTAATTAT	743
Db	121	CCCCCTCCCTCCATGCTCATCTCCCGCGCCCTCCAGTCATGTCGCGACAGGTTAAAAAT	180
QY	744	CAGTACCTTCGGGGCTATTCTCACACAACTTCCCACTCCCACTGTTTAAATAGTTTCCAG	803
Db	181	CAGTACCTTCGGGGCTATTCTCACACAACTTCCCACTCCCACTGTTTAAATAGTTTCCAG	240
QY	804	AACAACCTTAGTTCTTCTGCCCCAGTGTAAATAACACAGCAGTAGTCCTCATTTCAGACAT	863
Db	241	AACAACCTTAGTTCTTCTGCCCCAGTGTAAATAACACAGCAGTAGTCCTCATTTCAGACAT	300
QY	864	CTCCCTCCATACCCACTCCCAAGGCTCCAGTGTAGAGAGAGTCCCCCAAGAAAGGCTGAAA	923
Db	301	CTCCCTCCATACCCACTCCCAAGGCTCCAGTGTAGAGAGAGTCCCCCAAGAAAGGCTGAAA	360
QY	924	CACATATGATGACCAACAGACCCGAGACACACAGTCATGCGCGAGGTGAGAGGCATCGGTCC	983
Db	361	CACATATGATGACCAACAGACCCGAGATCACAGTCATGCGCGAGGTGAGAGGCATCGGTCC	420
QY	984	CTGGATCGCGGGGACGAGGCGCAGTCCCGACAGGAGAAGACAAGACAGCGGTACAGA	1043
Db	421	CTGGATCGCGGGGACGAGGCGCAGTCCCGACAGGAGAAGACAAGACAGCGGTACAGA	480
QY	1044	TCTGATTTATGACCGAGGAGGAACACATCTTCGCCACCGCAGCTACGAACGGAGCAGAGAG	1103
Db	481	TCTGATTTATGACCGAGGAGGAACACATCTTCGCCACCGCAGCTACGAACGGAGCAGAGAG	536
QY	1104	CGAGAACGGGAGAGACACAGGCATCGAGACACCGAAGATCACCATCTCTGGAAGGTCC	1163
Db	537	-----	536
QY	1164	TACAAAAAGAGTATAGAGATCTGGNAGGAGTTACGGTTTATCGGTTTCTTCTGAACT	1223
Db	537	-----	536
QY	1224	GCTGGATGCACACAGAATTACTCGGGGAGATTATTAANAATACAGATTCTTGGGCCCA	1283
Db	537	-----	536
QY	1284	CCCCTGGAGTTGTGAATCATCGCTCCCCAAGTAGGGAGAGAAGAGAGAGCTCGTTGGGAG	1343
Db	537	-----TCGCTCCCNAGTAGGAGAGAGAAGAGAGCTCGTTGGGAG	576
QY	1344	GAAGAAAAAGCCGTTGGAGTGACAAACAGAGTTCTTGGCAAGAACAAGAACTATACCTCA	1403
Db	577	GAAGAAAAAGCCGTTGGAGTGACAAACAGAGTTCTTGGCAAGAACAAGAACTATACCTCA	636

QY	2484	ACGAAACCAAGCTCTGTCCTGATCGATCACTCGATCGTGAACAGTTCACCCCGATGTC	2543
Db	1717	ACGAAACCAAGCTCTGTCCTGATCGATCACTCGATCGTGAACAGTTCACCCCGATGTC	1776
QY	2544	ATTACTTTTCCGATTAATCGTCCACTTTGGGATACGCGCTGCACAGATTGAGTTATGACGGA	2603
Db	1777	ATTACTTTTCCGATTAATCGTCCACTTTGGGATACGCGCTGCACAGATTGAGTTATGACGGA	1836
QY	2604	GACCCACAGTACCAAAACCTGTGGAGAGATTATGTGAACCTTCGCCACCTCTCTAGCAAAAT	2663
Db	1837	GACCCACAGTACCAAAACCTGTGGAGAGATTATGTGAACCTTCGCCACCTCTCTAGCAAAAT	1896
QY	2664	AGTCCCAAGTCAAAACCTGTGAAGAGATTATGTGAACCTTCGCCACCTCTCTAGCAAAAT	2723
Db	1897	AGTCCCAAGTCAAAACCTGTGAAGAGATTATGTGAACCTTCGCCACCTCTCTAGCAAAAT	1956
QY	2724	AAATACGGCAGAAAGTAACAATGAGACGAGAAAGTAAACGCTGAGCTTAAGTAGCCAAGGA	2783
Db	1957	AAATACGGCAGAAAGTAACAATGAGACGAGAAAGTAAACGCTGAGCTTAAGTAGCCAAGGA	2016
QY	2784	TTCTGAAAACTGGCATCCGCTTCTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCT	2843
Db	2017	TTCTGAAAACTGGCATCCGCTTCTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCT	2076
QY	2844	ACCATCATATCCGCTACCAACCAATGCTTAATGCAATTTGGACAAGTTGATAGGATATCT	2903
Db	2077	ACCATCATATCCGCTACCAACCAATGCTTAATGCAATTTGGACAAGTTGATAGGATATCT	2136
QY	2904	TTCCAAGATCGTTGCTGTGAGCTGGCCATGACCTCATCCAAAGTCAATCAATTTAAATTTT	2963
Db	2137	TTCCAAGATCGTTGCTGTGAGCTGGCCATGACCTCATCCAAAGTCAATCAATTTAAATTTT	2196
QY	2964	GGATGAAATCTGATCATGCGAGAAATTCATTAATCTAATCTGTGGAATTCGGCAGCCCAAA	3023
Db	2197	GGATGAAATCTGATCATGCGAGAAATTCATTAATCTAATCTGTGGAATTCGGCAGCCCAAA	2256
QY	3024	TACGGAGACAGAAAGTTCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3083
Db	2257	TACGGAGACAGAAAGTTCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2316
QY	3084	AATATCATGTCAGCTTGGCCAAAGATGACCAACTCCCTCGAGGATTAACCAATGAA	3143
Db	2317	AATATCATGTCAGCTTGGCCAAAGATGACCAACTCCCTCGAGGATTAACCAATGAA	2376
QY	3144	CGGTTGGAAATTCCTGGGTGATGCTGTTGTTGAATTTCTGACACGCTCCATTTGTACTAT	3203
Db	2377	CGGTTGGAAATTCCTGGGTGATGCTGTTGTTGAATTTCTGACACGCTCCATTTGTACTAT	2436
QY	3204	TTGTTTCTAGTCTGGAAGAGGATTTAGCAACCTATCGGACTGCAATTTGTTCAGAAAT	3263
Db	2437	TTGTTTCTAGTCTGGAAGAGGATTTAGCAACCTATCGGACTGCAATTTGTTCAGAAAT	2496
QY	3264	CAGCACTTGCATGCTAGCAAGAAATTTGAACTGATGATGATGATGATGATGATGATGATGATGAT	3323
Db	2497	CAGCACTTGCATGCTAGCAAGAAATTTGAACTGATGATGATGATGATGATGATGATGATGATGAT	2556
QY	3324	GGGCTTGAACCTTTGTAGAGAAATCGGACCTTTCGACATGCAATGCGCAATTTGTAAGCG	3383
Db	2557	GGGCTTGAACCTTTGTAGAGAAATCGGACCTTTCGACATGCAATGCGCAATTTGTAAGCG	2616
QY	3384	TTAATAGGAGCTTTTACTTGGAGGAAAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3443
Db	2617	TTAATAGGAGCTTTTACTTGGAGGAAAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2676
QY	3444	TTGCTCTTAAATGATCGGACCTGCGGAGTCTGGCTCAATTTATCTCTCCACCCACTC	3503
Db	2677	TTGCTCTTAAATGATCGGACCTGCGGAGTCTGGCTCAATTTATCTCTCCACCCACTC	2736
QY	3504	CAACTACAAGGACCAATCTGATCGCAACTTTATTTGAACTTCTCCAGTTCTTACAAAAA	3563
Db	2737	CAACTACAAGGACCAATCTGATCGCAACTTTATTTGAACTTCTCCGGTTCTTACAAAAA	2796
QY	3564	CTTACTGAGTTTGAAGCAATTTGGAGTAATTTTTTACTCATGTTCTGCACTTCTTGGCAAGG	3623

Db	2797	CTTACTGAGTTTGAAGCAATTTGGAGTAATTTTTTACTCATGTTTGACTTCTGGCAAGG	2856
QY	3624	GCATTCACATTTGAGAACTGTGGGATTTAAACCATCTGACCCCTAGGCCACCAATCAGAGAAATG	3683
Db	2857	GCATTCACATTTGAGAACTGTGGGATTTAAACCATCTGACCCCTAGGCCACCAATCAGAGAAATG	2916
QY	3684	GAATTCCTAGGTGACTCCATTAATGCAACTGTGTAGCCACAGAGTACTTATTCATTCATTTTC	3743
Db	2917	GAATTCCTAGGTGACTCCATTAATGCAACTGTGTAGCCACAGAGTACTTATTCATTCATTTTC	2976
QY	3744	CCAGATCATCATGAGGACACTTAACTTTGTTGCGAAGCTCTTTGGTGAATAATAGAACT	3803
Db	2977	CCAGATCATCATGAGGACACTTAACTTTGTTGCGAAGCTCTTTGGTGAATAATAGAACT	3036
QY	3804	CAGGCCAAGGTAGCGGAGGAGCTGGGCATGCGAGGAGTACGCCATNACCACGACCAAGACC	3863
Db	3037	CAGGCCAAGGTAGCGGAGGAGCTGGGCATGCGAGGAGTACGCCATNACCACGACCAAGACC	3096
QY	3864	AAGAGCCCTGTGGCGCTTCGCACCAAGACCTTTGGCGGACCTTTTGGAAATCATTTATTGCA	3923
Db	3097	AAGAGCCCTGTGGCGCTTCGCACCAAGACCTTTGGCGGACCTTTTGGAAATCATTTATTGCA	3156
QY	3924	GGCTCTACACTGATAAGGATTTGGAAATGTTTTCATCTTTCATGATGTTCTGCTCTCTTT	3983
Db	3157	GGCTCTACACTGATAAGGATTTGGAAATGTTTTCATCTTTCATGATGTTCTGCTCTCTTT	3216
QY	3984	CCACGATTTGAAAGAAATTTCAATTTTGAATCAGGATTTGAATGACCCCAAAATCCCAAGCTTCAG	4043
Db	3217	CCACGATTTGAAAGAAATTTCAATTTTGAATCAGGATTTGAATGACCCCAAAATCCCAAGCTTCAG	3276
QY	4044	CAGTGTGCTGACACTTAGGACAGAAAGGAAAGAGCCAGACATTCCTCTGTACAAGACT	4103
Db	3277	CAGTGTGCTGACACTTAGGACAGAAAGGAAAGAGCCAGACATTCCTCTGTACAAGACT	3336
QY	4104	CTGCAGACAGTGGGCCCCATCCCATGCCGAACTTATTCAGCAAGCGGAAATTTTCAAGGGA	4163
Db	3337	CTGCAGACAGTGGGCCCCATCCCATGCCGAACTTATTCAGCAAGCGGAAATTTTCAAGGGA	3396
QY	4164	GAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTTTCAGCAAGCGGAAATTTGGAGCAGCAATG	4223
Db	3397	GAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTTTCAGCAAGCGGAAATTTGGAGCAGCAATG	3456
QY	4224	GATGCGCTTGAATAATAATTAATTTTCCAGATGCGCCATCAGAAAGCGGTTTCATCGAACGG	4283
Db	3457	GATGCGCTTGAATAATAATTAATTTTCCAGATGCGCCATCAGAAAGCGGTTTCATCGAACGG	3516
QY	4284	AACTACAGACAGAGGTTTAAAGAAATGAGGTGGGAAAGAGGAGCATCAAGAGAGAGGCCA	4343
Db	3517	AACTACAGACAGAGGTTTAAAGAAATGAGGTGGGAAAGAGGAGCATCAAGAGAGAGGCCA	3576
QY	4344	GATGAGACTGAAGACATCAAGAAATAA 4370	
Db	3577	GATGAGACTGAAGACATCAAGAAATAA 3603	

RESULT 11

AAH13924

ID AAH13924 standard; cDNA; 2598 BP.

XX AAH13924;

XX XX

DT 26-JUN-2001 (first entry)

XX Human cDNA sequence SEQ ID NO:10948.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

XX OS

XX PN BP1074617-A2.

XX PD 07-FEB-2001.

XX 28-JUL-2000; 2000EP-00116126.
XX 29-JUL-1999; 99JP-00248036.
XX 29-JUL-1999; 99JP-00300253.
XX 11-AUG-1999; 99JP-00118776.
XX 11-JAN-2000; 2000JP-00118776.
XX 02-MAY-2000; 2000JP-00183767.
XX 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
XX length cDNAs defined in the specification, and for the detection and/or
XX diagnosis of the abnormality of the proteins encoded by the full-length
XX cDNAs.
XX
XX Claim 8; SEQ ID NO 10948; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
XX length cDNAs defined in the specification. Where a primer set comprises:
XX (a) an oligo-dT primer and an oligonucleotide complementary to the
XX complementary strand of a polynucleotide which comprises one of the 5602
XX nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in the
XX specification. The primer sets can be used in antisense therapy and in
XX gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
XX represent human amino acid sequences; and AAH13629 to AAH13632 represent
XX oligonucleotides, all of which are used in the exemplification of the
XX present invention
XX
XX Sequence 2598 BP; 766 A; 543 C; 592 G; 697 T; 0 U; 0 Other;
SQ
Query Match 54.2%; Score 2582; DB 4; Length 2598;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2588; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2052 GGATTTTCTATGTTGCACATGCCCTCCCTGACCAATATTCACCTGTGTAAAGTAATTAGA 2111
DB 1 GGATTTTCTATGTTGCACATGCCCTCCCTGACCAATATTCACCTGTGTAAAGTAATTAGA 60
QY 2112 TTCACATAGACTACACGATTCATTTTCATGAAGATGATGCCGAGAAATTTTGTGTG 2171
DB 61 TTCAACATAGACTACACGATTCATTTTCATGAAGATGATGCCGAGAAATTTTGTGTG 120
QY 2172 AAAGGCTTGAACCTTTTTCACCTGTTCCCTATTTCAGAGATATTTTGAATTTATATGACTGG 2231
DB 121 AAAGGCTTGAACCTTTTTCACCTGTTCCCTATTTCAGAGATATTTTGAATTTATATGACTGG 180
QY 2232 AATCTTTAAAGGCTCTTTTGTGTGAAGACAGCCCTCCCTGCTGCCCAAGATTTTCATTTTCATG 2291
DB 181 AATCTTTAAAGGCTCTTTTGTGTGAAGACAGCCCTCCCTGCTGCCCAAGATTTTCATTTTCATG 240
QY 2292 CCACGTTTGTGAAGATTTCTTCAGATGAGGAAGGAAGTGTCTGTCATGACCAAGATT 2351
DB 241 CCACGTTTGTGAAGATTTCTTCAGATGAGGAAGGAAGTGTCTGTCATGACCAAGATT 300
QY 2352 CTCTGTACTTGTAAAGTGCAGCAAGGCCCTGGTGCCTGAGGAGGATTTGCCAATATG 2411

DB 301 CTCTGTACTTGTAAAGTGCAGCAAGGCCCTGGTGCCTGAGGAGGATTTGCCAATATG 360
QY 2412 CTTCAAGTGGGAGGAGCTGGAGTGGCAGAAATATGAGAGAGATGCAAAAGGCATGTTGTT 2471
DB 361 CTTCAAGTGGGAGGAGCTGGAGTGGCAGAAATATGAGAGAGATGCAAAAGGCATGTTGTT 420
QY 2472 AGCAACCCCTGGGAGCAAAACCAAGCTCTGTCCGTATTCGATCAACTGGATCGTGAACAGTTTC 2531
DB 421 AGCAACCCCTGGGAGCAAAACCAAGCTCTGTCCGTATTCGATCAACTGGATCGTGAACAGTTTC 480
QY 2532 AACCCCGATGTCATTTATCTTTTCCGATTAATCGTCCACTTTTGGGATAGCGCCTGCAACAGTTTG 2591
DB 481 AACCCCGATGTCATTTATCTTTTCCGATTAATCGTCCACTTTTGGGATAGCGCCTGCAACAGTTTG 540
QY 2592 AGTTATGAGGAGAGCCACAGTACCAAAACCTGTGGAAGAGTTATGTGAAACTTTCGCCAC 2651
DB 541 AGTTATGAGGAGAGCCACAGTACCAAAACCTGTGGAAGAGTTATGTGAAACTTTCGCCAC 600
QY 2652 CTCCTAGCAAAATAGTCCCAAGTCAAAACCTGCAAAACAGAAAGCTGCGACAGAGGGAG 2711
DB 601 CTCCTAGCAAAATAGTCCCAAGTCAAAACCTGCAAAACAGAAAGCTGCGACAGAGGGAG 660
QY 2712 GAAGCCCTCCAAAAAATACGGCAGAGAAATACAATGAGACGAGAAATACCGTGGAGCTA 2771
DB 661 GAAGCCCTCCAAAAAATACGGCAGAGAAATACAATGAGACGAGAAATACCGTGGAGCTA 720
QY 2772 AGTAGCAAGGATTTGGNAACTGGCATCCCTCTGTGATGTTCTGTCAGCATGCAATGATG 2831
DB 721 AGTAGCAAGGATTTGGNAACTGGCATCCCTCTGTGATGTTCTGTCAGCATGCAATGATG 780
QY 2832 CTACCTGTTCTCACCCATCATATCGCTACCAACCAATGCTTAATGATTTGACAAAGTTG 2891
DB 781 CTACCTGTTCTCACCCATCATATCGCTACCAACCAATGCTTAATGATTTGACAAAGTTG 840
QY 2892 ATAGGATATACCTTTCCAAAGATCGTTGTCTGTGTCAGCTGGCCATGATCATCAAGTCAT 2951
DB 841 ATAGGATATACCTTTCCAAAGATCGTTGTCTGTGTCAGCTGGCCATGATCATCAAGTCAT 900
QY 2952 CATTTAAATTTTGGATGATGATCTGATCATGCCAGGATTTCAATTAATCTAACTGTGAAAT 3011
DB 901 CATTTAAATTTTGGATGATGATCTGATCATGCCAGGATTTCAATTAATCTAACTGTGAAAT 960
QY 3012 CGGCGACCCAAATACGGGACAGAGAAAGTTTCATCATCATGACATCGGAGAGAAAGGATTT 3071
DB 961 CGGCGACCCAAATACGGGACAGAGAAAGTTTCATCATCATGACATCGGAGAGAAAGGATTT 1020
QY 3072 AACACCTTGATAAATATATCATGTACGCCCTTGCCCAAGATGACCCCACTCCCTCGAGGATTT 3131
DB 1021 AACACCTTGATAAATATATCATGTACGCCCTTGCCCAAGATGACCCCACTCCCTCGAGGATTT 1080
QY 3132 AACCAATGAAAGGTTGGAATTTCTGGGTGATGCTGTTGTGNAATTTCTGACCCAGCTC 3191
DB 1081 AACCAATGAAAGGTTGGAATTTCTGGGTGATGCTGTTGTGNAATTTCTGACCCAGCTC 1140
QY 3192 CATTTGTACTATTGTTTCTTAGTCTGGAAGAGGAGGATTTAGCAACCTATCGGACTGCC 3251
DB 1141 CATTTGTACTATTGTTTCTTAGTCTGGAAGAGGAGGATTTAGCAACCTATCGGACTGCC 1200
QY 3252 ATTTGTTCAGAATCAGCACCTTCCATGCTAGCAAAAGAAACTTTGAACTGGATCCATTTATG 3311
DB 1201 ATTTGTTCAGAATCAGCACCTTCCATGCTAGCAAAAGAAACTTTGAACTGGATCCATTTATG 1260
QY 3312 CTGTATGCTCAGGGCTGACCTTTGTAGAGATGCGACCTTCGACATGCAATGGCCAAT 3371
DB 1261 CTGTATGCTCAGGGCTGACCTTTGTAGAGATGCGACCTTCGACATGCAATGGCCAAT 1320
QY 3372 TGTGTTTGAAGCTTTAATAGAGCTGTTTACTTTGGAGGGAGGCTGGAGGAAGCAAGCAG 3431
DB 1321 TGTGTTTGAAGCTTTAATAGAGCTGTTTACTTTGGAGGGAGGCTGGAGGAAGCAAGCAG 1380
QY 3432 TTATTGTCAGCTTCTCTTTAATGATCGGACCTGCGGAAAGTCTGGCTCAATTTATCTT 3491

Db 1381 TTATTTGGAGCGTTGCTCTTTAATGATCGGACCTCGCGAAGCTCTGGCTCAATTATCCT 1440
Qy 3492 CTCACCCCACTCAACTACAGAGCCAAATACGTGATCGCAACCTTATTTGAAACCTTCTCCA 3551
Db 1441 CTCACCCCACTCAACTACAGAGCCAAATACGTGATCGCAACCTTATTTGAAACCTTCTCCG 1500
Qy 3552 GTTCTACAAAACCTTACTGAGTTTGAAGCAATTTGGAGTAAATTTTACTCATGTTTCCA 3611
Db 1501 GTTCTACAAAACCTTACTGAGTTTGAAGCAATTTGGAGTAAATTTTACTCATGTTTCCA 1560
Qy 3612 CTTCTGCGAAGGCAATTCACATTTGAGAACTGTGGGATTTAAACCATCTGACCCCTAGGCCAC 3671
Db 1561 CTTCTGCGAAGGCAATTCACATTTGAGAACTGTGGGATTTAAACCATCTGACCCCTAGGCCAC 1620
Qy 3672 AATCAGAGAAATGAATCTTAGTGATCTCCATTAATGCAACTGTGTGACGACAGAGTACTTA 3731
Db 1621 AATCAGAGAAATGAATCTTAGTGATCTCCATTAATGCAACTGTGTGACGACAGAGTACTTA 1680
Qy 3732 TTTCAATTCATTTCCAGATCATCATGAGGACACTTAACCTTTGTTGGAAGCTCTTTGGTG 3791
Db 1681 TTTCAATTCATTTCCAGATCATCATGAGGACACTTAACCTTTGTTGGAAGCTCTTTGGTG 1740
Qy 3792 AATAATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGGATCGAGGAGTACGCCATAACC 3851
Db 1741 AATAATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGGATCGAGGAGTACGCCATAACC 1800
Qy 3852 AACGACAGCAAGAGGCTGTGGCGCTTTCGCAACAGACCTTGGCGGACCTTTTGGAA 3911
Db 1801 AACGACAGCAAGAGGCTGTGGCGCTTTCGCAACAGACCTTGGCGGACCTTTTGGAA 1860
Qy 3912 TCATTTATTTGCGCGCTGTACACTGATTAAGGATTTGGAAATGTTTCATCTTTTCATGAT 3971
Db 1861 TCATTTATTTGCGCGCTGTACACTGATTAAGGATTTGGAAATGTTTCATCTTTTCATGAT 1920
Qy 3972 GTCTGCTCTTTCCAGCATTTGAAGAAATTCATTTTGAATCAGGATTTGAATGACCCCAAA 4031
Db 1921 GTCTGCTCTTTCCAGCATTTGAAGAAATTCATTTTGAATCAGGATTTGAATGACCCCAAA 1980
Qy 4032 TCCAGCTTTCAGCAGTGTGCTTGACATTTAGGACAGAGGAAAGAGCCAGACATTCCT 4091
Db 1981 TCCAGCTTTCAGCAGTGTGCTTGACATTTAGGACAGAGGAAAGAGCCAGACATTCCT 2040
Qy 4092 CTGTACAGACTCTGACAGCAGTGGGCCCCATCCATCCCGAACCTTACACTGTGGCTGTT 4151
Db 2041 CTGTACAGACTCTGACAGCAGTGGGCCCCATCCATCCCGAACCTTACACTGTGGCTGTT 2100
Qy 4152 TATTTTCAAGGAGAAAGATAGGCTGTGGAAAGGACCAAGTATTCAGCAAGCGGAAATG 4211
Db 2101 TATTTTCAAGGAGAAAGATAGGCTGTGGAAAGGACCAAGTATTCAGCAAGCGGAAATG 2160
Qy 4212 GGAGCAGCAATGAGTGGCTTGAATAATATAATTTTCCAGATGCCCATCAGAGCGG 4271
Db 2161 GGAGCAGCAATGAGTGGCTTGAATAATATAATTTTCCAGATGCCCATCAGAGCGG 2220
Qy 4272 TTTATCGAAGCAAGTACAGACAGAGTATAAGAAATGAGTGGGAAAGAGAGCATCAA 4331
Db 2221 TTTATCGAAGCAAGTACAGACAGAGTATAAGAAATGAGTGGGAAAGAGAGCATCAA 2280
Qy 4332 GAGAGAGCCAGATGAGACTGAAGACATCAAGAAATAAGGAGGCGCATGCAAGTGTGGA 4391
Db 2281 GAGAGAGCCAGATGAGACTGAAGACATCAAGAAATAAGGAGGCGCATGCAAGTGTGGA 2340
Qy 4392 GTATTTACTTGTCTAGTAACTGTGACTGTGTCTATTGAGACCTAGCTAGTTTCTCTGC 4451
Db 2341 GTATTTACTTGTCTAGTAACTGTGACTGTGTCTATTGAGACCTAGCTAGTTTCTCTGC 2400
Qy 4452 AGCAATGAAGCAAGTGTGCTCATTTGAATAATAAATACAGAGTCAAAATCGCTATTGTGTT 4511
Db 2401 AGCAATGAAGCAAGTGTGCTCATTTGAATAATAAATACAGAGTCAAAATCGCTATTGTGTT 2460
Qy 4512 TTAATGATCTGTTTTAGTGGATGCTTTTATACAAAGTATTAGATTTTTTCTTCTATT 4571
Db 2461 TTAATGATCTGTTTTAGTGGATGCTTTTATACAAAGTATTAGATTTTTTCTTCTATT 2520

Qy 4572 TAACGAAAACCTGACTTTGGTGAATGTGCATTAATCTCTTTTATTTGCTCTTTAAATA 4631
Db 2521 TAACGAAAACCTGACTTTGGTGAATGTGCATTAATCTCTTTTATTTGCTCTTTAAATA 2580
Qy 4632 ATAAAATTCAAGAAGCAT 4649
Db 2581 ATAAAATTCAAGAAGCAT 2598

RESULT 12

AEA20644
ID AEA20644 standard; cDNA; 1784 BP.

XX AEA20644;

XX DT 11-AUG-2005 (first entry)

XX Novel human polynucleotide SEQ ID NO 1338.

XX vulnary; CNS-gen.; gene therapy; diagnostic; forensic; mapping;
XX DNA purification; protein purification; osteoarthritis; antiarthritic;
XX osteopathic; musculoskeletal disease; osteoporosis; endocrine disease;
XX periodontal disease; antiinflammatory; mouth disease; burns; injury;
XX peripheral neuropathy; alzheimers disease; neuroprotective; nootropic;
XX degeneration; parkinsons disease; antiparkinsonian; neurological disease;
XX cerebrovascular ischemia; cerebroprotective; vasotropic;
XX cardiovascular disease; autoimmune disease; immunosuppressive;
XX immune disorder; viral infection; virucide; infection; cancer;
XX cytostatic; neoplasm; ss.

XX Homo sapiens.

XX WO2005049806-A2.

XX 02-JUN-2005.

XX 11-MAR-2004; 2004WO-US007412.

XX 14-MAR-2003; 2003US-00389559.

XX (NUVE-) NUVELO INC.

XX Tang TY, Wang J, Wang ZW, Zhang J, Ren F, Zhou P, Ma Y;

PI Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;

PI Wehrman T, Weng G, Boyle B;

XX WPI; 2005-417730/42.

XX New polynucleotide encoding a polypeptide with biological activity,
XX useful for treating a disease or disorder, e.g. osteoarthritis, burns,
XX CNS and peripheral disease, stroke, autoimmune disorders, viral
XX infection, or cancer.

XX Example 3; SEQ ID NO 1338; 500pp; English.

XX The invention describes a new isolated polynucleotide (I) encoding a
XX polypeptide with biological activity comprising: a nucleotide sequence of
XX SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes
XX to the sequence of (i) under stringent hybridization conditions; or a
XX nucleotide sequence having greater than 99% sequence identity with the
XX sequence of (i). Also described are: a(n) (expression)vector comprising
XX (I); a host cell genetically engineered to comprise (I) operatively,
XX associated with a regulatory sequence that modulates expression of the
XX polynucleotide in the host cell; an isolated polypeptide comprising a
XX sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide
XX is: a polypeptide encoded by (i); or a polypeptide encoded by a
XX polynucleotide hybridizing under stringent conditions with any one of SEQ
XX ID NOS: 1-567; a composition comprising the polypeptide of (3) and a
XX carrier; an antibody directed against the polypeptide of (3); a method
XX for detecting (I) in a sample; a method for detecting the polypeptide of
XX (3) in a sample; a method for identifying a compound that binds to the
XX polypeptide of (3); a method of producing the polypeptide of (3); and a

CC collection of polynucleotides, where the collection comprising of at
CC least one of SEQ ID NOS: 1-567. (I) is a polynucleotide comprising any of
CC the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological
CC activity, which comprises any of the amino acid sequence of SEQ ID NOS:
CC 568-1134. All sequences are fully defined in the specification. The
CC sequences and methods are useful in diagnostics, forensic, and gene
CC mapping, in identifying of mutations responsible for genetic disorders or
CC other traits, in assessing biodiversity, and for producing many other
CC types of data and products dependent on DNA and amino acid sequences. The
CC composition and method are useful for treating a disease or disorder,
CC e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
CC peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
CC autoimmune disorders, viral infection, or cancer. This sequence
CC represents a novel polynucleotide of the invention.

XX
SQ Sequence 1784 BP; 536 A; 363 C; 405 G; 480 T; 0 U; 0 Other;

Query Match 36.4%; Score 1735.6; DB 14; Length 1784;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 1747; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY	2901	ACTTCCAGATCGTGTCTGTGTGGAGCTGGCCATGCACTCATCCAAGTCATCATTTAAAT	2960
DB	14	ACCTTGTAATACATGGTCCGGCCAGCTGGCCATGCACTCATCCAAGTCATCATTTAAAT	73
QY	2961	TTTGGAAATCAATCTCATGATGCGAGAAATTCATTAATCTAACTGTGGAATTCGGAGCCC	3020
DB	74	TTTGGAAATCAATCTCATGATGCGAGAAATTCATTAATCTAACTGTGGAATTCGGAGCCC	133
QY	3021	AAATCGGAGACAGAAAGTTTCATCATGCAATGCGGAAGAAAGGATTAACACCTTG	3080
DB	134	AAATCGGAGACAGAAAGTTTCATCATGCAATGCGGAAGAAAGGATTAACACCTTG	193
QY	3081	ATAATATATCATGTCAGCCCTTGGCCAGATGACCCAACTCCCTCGAGGATTAACCAAT	3140
DB	194	ATAATATATCATGTCAGCCCTTGGCCAGATGACCCAACTCCCTCGAGGATTAACCAAT	253
QY	3141	GAACGGTTCGAATTCCTGGGTGATGCTGTGTTGAAATTTCTGACAGCGCTCCATTTGTAC	3200
DB	254	GAACGGTTCGAATTCCTGGGTGATGCTGTGTTGAAATTTCTGACAGCGCTCCATTTGTAC	313
QY	3201	TATTTGTTTCTAGTCTGGAAGAGGAGGATAGCAACCTATCGGCTGCCATTTGTTGAG	3260
DB	314	TATTTGTTTCTAGTCTGGAAGAGGAGGATAGCAACCTATCGGCTGCCATTTGTTGAG	373
QY	3261	AATCAGCACTTGCATGTCAGCAAGAAACTTTGAATCGAATCCATTTATGCTGTATGCT	3320
DB	374	AATCAGCACTTGCATGTCAGCAAGAAACTTTGAATCGAATCCATTTATGCTGTATGCT	433
QY	3321	CAGGGCCTGACCTTTGTAGAGAACTCGACCTTCGACATGCAATGCCAATTTGTTTGA	3380
DB	434	CAGGGCCTGACCTTTGTAGAGAACTCGACCTTCGACATGCAATGCCAATTTGTTTGA	493
QY	3381	GCCTTAATAGGAGCTGTTTACTTGGAGGAGGCTGGAGGAAGCCCAAGCAGTTATTGGA	3440
DB	494	GCCTTAATAGGAGCTGTTTACTTGGAGGAGGCTGGAGGAAGCCCAAGCAGTTATTGGA	553
QY	3441	CGTTGCTCTTTAATGATCGGAGCTTGGGAAAGTCTGGCTCAATTTATGCTCTCCACCA	3500
DB	554	CGTTGCTCTTTAATGATCGGAGCTTGGGAAAGTCTGGCTCAATTTATGCTCTCCACCA	613
QY	3501	CTCCAACTACAGAGCCAAATCTGATCGCAACTTTATTGAACCTTCTCCAGTTCTACAA	3560
DB	614	CTCCAACTACAGAGCCAAATCTGATCGCAACTTTATTGAACCTTCTCCAGTTCTACAA	673
QY	3561	AAACTTACTGAGTTTGAAGAGCAATTTGGAGTAATTTTACTCATGTTGCACTTCTGGCA	3620
DB	674	AAACTTACTGAGTTTGAAGAGCAATTTGGAGTAATTTTACTCATGTTGCACTTCTGGCA	733
QY	3621	AGGGCAATTCATTTGAGAACTGTGGGATTTAAACCATCTGACCCCTAGGCCCAATTCAGAA	3680
DB	734	AGGGCAATTCATTTGAGAACTGTGGGATTTAAACCATCTGACCCCTAGGCCCAATTCAGAA	793

RESULT 13

ACF25385

ID ACF25385 standard; DNA; 1626 BP.

XX

QY	3681	ATGGAATTCCTAGGTGAGCTCCATAATGCAACTGGTAGCCACAGAGTACTTATTTCATCAT	3740
DB	794	ATGGAATTCCTAGGTGAGCTCCATAATGCAACTGGTAGCCACAGAGTACTTATTTCATCAT	853
QY	3741	TTTCCAGATCATCATGAGGACACATTAATTTTGGCGAAGCTCTTTGGTGAATATAGA	3800
DB	854	TTTCCAGATCATCATGAGGACACATTAATTTTGGCGAAGCTCTTTGGTGAATATAGA	913
QY	3801	ACTCAGGCGCAAGGTAGCGGAGGAGCTGGGCATGCGAGGAGTAGCCCATACCAACGACAAG	3860
DB	914	ACTCAGGCGCAAGGTAGCGGAGGAGCTGGGCATGCGAGGAGTAGCCCATACCAACGACAAG	973
QY	3861	ACCAAGAGCCCTGTGCGCGCTTCGCAACAGACCTTTGGCGGACCTTTTGGAAATCATTTAT	3920
DB	974	ACCAAGAGCCCTGTGCGCGCTTCGCAACAGACCTTTGGCGGACCTTTTGGAAATCATTTAT	1033
QY	3921	GCAGCGCTGTACATGATTAAGGATTTGGNATATGTTTCATCTTTCATGAATCTCTGCTTC	3980
DB	1034	GCAGCGCTGTACATGATTAAGGATTTGGNATATGTTTCATCTTTCATGAATCTCTGCTTC	1093
QY	3981	TTTCCACGATTCGAAAGAAATTCATTTTGAATCAGGATTTGGAATGACCCCAAAATCCAGCTT	4040
DB	1094	TTTCCACGATTCGAAAGAAATTCATTTTGAATCAGGATTTGGAATGACCCCAAAATCCAGCTT	1153
QY	4041	CAGCAGTGTGCTTGACACTTGAAGACAGAAAGAGCCAGACATTCCTCTGTACAAG	4100
DB	1154	CAGCAGTGTGCTTGACACTTGAAGACAGAAAGAGCCAGACATTCCTCTGTACAAG	1213
QY	4101	ACTCTGCAGACAGTGGGCCCATCCCATGCCGAACTACACTGTGCTGCTTTTATTTCAAG	4160
DB	1214	ACTCTGCAGACAGTGGGCCCATCCCATGCCGAACTACACTGTGCTGCTTTTATTTCAAG	1273
QY	4161	CGAGAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTTCAGCAAGCGGAAATGGAGCAGCA	4220
DB	1274	CGAGAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTTCAGCAAGCGGAAATGGAGCAGCA	1333
QY	4221	ATGGAATGCGCTTGAATAATATATTTTCCAGATGGGCCCATCAGAAAGCGGTTTCATCGAA	4280
DB	1334	ATGGAATGCGCTTGAATAATATATTTTCCAGATGGGCCCATCAGAAAGCGGTTTCATCGAA	1393
QY	4281	CGGAAGTACAGACAGAGTTAAAGAAATGAGGTGGGAAAGAGGAGCATCAAGAGAGAGAG	4340
DB	1394	CGGAAGTACAGACAGAGTTAAAGAAATGAGGTGGGAAAGAGGAGCATCAAGAGAGAGAG	1453
QY	4341	CCAGATGAGACTGGAAGACATCAAGAAATAAGAGGAGGAGTGAAGTGTGGAGTATTACT	4400
DB	1454	CCAGATGAGACTGGAAGACATCAAGAAATAAGAGGAGGAGTGAAGTGTGGAGTATTACT	1513
QY	4401	TGCTCAGTAACCTGTGACTGTCTTATTCAGACCTAGCCTAGTTTCTTCGACAGCAATGA	4460
DB	1514	TGCTCAGTAACCTGTGACTGTCTTATTCAGACCTAGCCTAGTTTCTTCGACAGCAATGA	1573
QY	4461	ACGAAGTGTCTCATTGAAATAAATACAGAGTCAAAATCGCTATTTGCTTTTAAATGATC	4520
DB	1574	ACGAAGTGTGTCTCATTGAAATAAATACAGAGTCAAAATCGCTATTTGCTTTTAAATGATC	1633
QY	4521	TGTTTTTACCTGATGCTCTTTTATTAACAAGTATTAGATTTTCTTCTATTAAACGGAAA	4580
DB	1634	TGTTTTTACCTGATGCTCTTTTATTAACAAGTATTAGATTTTCTTCTATTAAACGGAAA	1693
QY	4581	ACTTGACTTTGGTGAATGTCATTAATCTCTTTTATTTTGGCTCTTTTAAATAATAAATTC	4640
DB	1694	ACTTGACTTTGGTGAATGTCATTAATCTCTTTTATTTTGGCTCTTTTAAATAATAAATTC	1753
QY	4641	AGAAGCATTTCTATGTCGAATAGA	4666
DB	1754	AGAAGCATTTCTATGTCGAATAGA	1779

AC ACF25385;
 XX 22-SEP-2003 (first entry)
 XX Human putative ribonuclease III gene.
 DE DE
 XX spinal cord; neuropathic pain; central sensitisation pain; pain;
 KW analgesic; gene therapy; gene; ss.
 KW OS
 XX Homo sapiens.
 XX EP1284298-A2.
 XX 19-FEB-2003.
 XX 26-JUL-2002; 2002EP-00255229.
 XX 27-JUL-2001; 2001GB-00018354.
 PR 07-FEB-2002; 2002GB-00002883.
 XX (WARN) WARNER LAMBERT CO.
 XX Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
 PI WPI: 2003-543489/52.
 DR P-PSDB; ABM04841.
 XX
 XX Use of an isolated gene sequence in the screening of compounds for
 PT diagnosing or treating pain.
 PT
 XX Claim 1; Page 185; 188pp; English.
 XX The invention relates to a novel isolated gene sequence that is
 CC downregulated in the spinal cord of a mammal in response to mechanically
 CC distinct first and second models of neuropathic or central sensitisation
 CC pain, useful in the screening of compounds for diagnosing or treating
 CC pain. A protein encoded by a gene of the invention has analgesic
 CC activity. A polynucleotide of the invention may have a use in gene
 CC therapy. The gene sequence is useful for preparing a composition for
 CC diagnosing or treating pain. The present sequence represents a gene of
 CC the invention
 XX
 XX Sequence 1626 BP; 484 A; 350 C; 379 G; 413 T; 0 U; 0 Other;
 SQ
 Query Match 34.0%; Score 1619.6; DB 9; Length 1626;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1622; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 2745 ATGAGACGAGAGTAACGGTGGAGCTAAGTAGCCAGGATTTCTGGAAAACCTGGCATCCGT 2804
 1 ATGAGACGAGAGTAACGGTGGAGCTAAGTAGCCAGGATTTCTGGAAAACCTGGCATCCGT 60
 2805 TCTGATGTCGTGACGATCAATGATGCTACCTGTTCTGACCCCATCATATCCGCTACCAC 2864
 61 TCTGATGTCGTGACGATCAATGATGCTACCTGTTCTGACCCCATCATATCCGCTACCAC 120
 2865 CAATGCTCAATGATTTGGACAAAGTTGATAGGATATACTTTCCAGATCGTTGTCGTGTTG 2924
 121 CAATGCTCAATGATTTGGACAAAGTTGATAGGATATACTTTCCAGATCGTTGTCGTGTTG 180
 2925 CAGCTGGCCATGACATCAATCAATCAATTAATTTTGGAAATGAATCCTGATCATGCC 2984
 181 CAGCTGGCCATGACATCAATCAATCAATTAATTTTGGAAATGAATCCTGATCATGCC 240
 2985 AGGAATTCATATCTTAACCTGGAATTCGGCAGCCCAATATCGGACAGAGAAAGTTTCA 3044
 241 AGGAATTCATATCTTAACCTGGAATTCGGCAGCCCAATATCGGACAGAGAAAGTTTCA 300
 3045 CACATGACATCGGAGAAAGGGATTAACACCTTGATAAATATCATGTCAAGCCCTTGGC 3104
 301 CACATGACATCGGAGAAAGGGATTAACACCTTGATAAATATCATGTCAAGCCCTTGGC 360
 3105 CAAGATGACCCCACTCCCTCGAGGATTAACCAATGAACGGTTGGAAATTCCTGGGTGAT 3164

361 CAAAGATGACCCAACTCCCTCGAGGATTAACCAATGAACGGTTGGAATTCCTGGGTGAT 420
 3165 GCTGTTGTTGAAATTTCTGACCAAGCGTCCATTTGTACTATTGTTGTTCTAGTCTGGAAGAA 3224
 421 GCTGTTGTTGAAATTTCTGACCAAGCGTCCATTTGTACTATTGTTGTTCTAGTCTGGAAGAA 480
 3225 GGAGGATTAGCAACCTATCGGACTGCCATTTGTCAGAAATCAGACACCTTGGCATGCTAGCA 3284
 481 GGAGGATTAGCAACCTATCGGACTGCCATTTGTCAGAAATCAGACACCTTGGCATGCTAGCA 540
 3285 AAGAAACTTTGAATCTGATCGATCCATTTATGCTGTATGCTCAGGGGCTGACCTTTGTAGAGAA 3344
 541 AAGAAACTTTGAATCTGATCGATCCATTTATGCTGTATGCTCAGGGGCTGACCTTTGTAGAGAA 600
 3345 TCGGACCTTTGACATGCAATGCGCAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTGT 3404
 601 TCGGACCTTTGACATGCAATGCGCAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTGT 660
 3405 GAGGGAGCTCGGAGGAGCAAGCAAGTATTATTGGACGCTTGTCTTTTAATGATCCGGAC 3464
 661 GAGGGAGCTCGGAGGAGCAAGCAAGTATTATTGGACGCTTGTCTTTTAATGATCCGGAC 720
 3465 CTGGCGAAGTCTGGCTCAATTTATCTCTCCACCTCAACTCAACTCAAGAGCCAAATACT 3524
 721 CTGGCGAAGTCTGGCTCAATTTATCTCTCCACCTCAACTCAACTCAAGAGCCAAATACT 780
 3525 GATCGCAACTTTATTGAAACTTTCTCCAGTTCTACAAAACTTACTGAGTTTGAAGAGCA 3584
 781 GATCGCAACTTTATTGAAACTTTCTCCGTTCTACAAAACTTACTGAGTTTGAAGAGCA 840
 3585 ATTGGAGTAAATTTTACTCATGTTGCACTTTCTGGCAAGGCAATTCATATGAGAACTGTG 3644
 841 ATTGGAGTAAATTTTACTCATGTTGCACTTTCTGGCAAGGCAATTCATATGAGAACTGTG 900
 3645 GATTTTAAACATCTGACCTTAGCCCAATCAGAGAAATGGAATTCCTAGTGTACTCCATA 3704
 901 GATTTTAAACATCTGACCTTAGCCCAATCAGAGAAATGGAATTCCTAGTGTACTCCATA 960
 3705 ATGCAACTGTTAGCCACAGAGTACTTTATTTCATTTCTCCAGATCATCATGAAGGACAC 3764
 961 ATGCAACTGTTAGCCACAGAGTACTTTATTTCATTTCTCCAGATCATCATGAAGGACAC 1020
 3765 TTAACTTTGTTGCGAAGCTCTTTGTTGTAATAATAGAACTCAGGCCAAGGTAGCGGAGGAG 3824
 1021 TTAACTTTGTTGCGAAGCTCTTTGTTGTAATAATAGAACTCAGGCCAAGGTAGCGGAGGAG 1080
 3825 CTGGGCATCGCAGGATGACCCATTAACCAAGCAAGCAAGCAAGGCGCTGTGGCGCTTCGC 3884
 1081 CTGGGCATCGCAGGATGACCCATTAACCAAGCAAGCAAGCAAGGCGCTGTGGCGCTTCGC 1140
 3885 ACCAAGACCTTGGCGGACCTTTTGGAAATCATTTATTGACGCGCTGTACACTGATAAGGAT 3944
 1141 ACCAAGACCTTGGCGGACCTTTTGGAAATCATTTATTGACGCGCTGTACACTGATAAGGAT 1200
 3945 TTGGAATATGTTTCATATCTTTTCATGATGTCGTTCTTTTCCAGATGAAGAAATTCATT 4004
 1201 TTGGAATATGTTTCATATCTTTTCATGATGTCGTTCTTTTCCAGATGAAGAAATTCATT 1260
 4005 TTGGAATCAGGATTTGGAATGACCCCAATCCAGCTTCCAGCTGTTGCTTGACACTTAGG 4064
 1261 TTGGAATCAGGATTTGGAATGACCCCAATCCAGCTTCCAGCTGTTGCTTGACACTTAGG 1320
 4065 ACAGAAAGGAAAAAGACCCAGACATTTCTCTGTATCAAGACTCTGTCAGACAGTGGGCCCATCC 4124
 1321 ACAGAAAGGAAAAAGACCCAGACATTTCTCTGTATCAAGACTCTGTCAGACAGTGGGCCCATCC 1380
 4125 CATGCCCGAACCTACATCTGTGGCTGTTTATTTCATGAGGAGAAAGAAATAGCTGTGGGAAA 4184
 1381 CATGCCCGAACCTACATCTGTGGCTGTTTATTTCATGAGGAGAAAGAAATAGCTGTGGGAAA 1440
 4185 GGACCAAGTATTTCAGCAAGCGGAAATGGGAGCAGCAATGGATGGCTTGGAAATTAAT 4244

Db 1441 GGACCAAGTATTTCAGAACGCGAAATGGAGCAGCAATGGATCGCTTCAAAAATATATAT 1500
Qy 4245 TTTCCCCAGATGCCCATCAGNAGCGGTTTCATCGAACGGAAGTACAGACAGATTAAAA 4304
Db 1501 TTTCCCCAGATGCCCATCAGAACGCGGTTTCATCGAACGGAAGTACAGACAGATTAAAA 1560
Qy 4305 GAAATGAGTGGGAAAGAGAGCATCAAGAGAGAGAGCCAGATGAGACTGAAGACATCAAG 4364
Db 1561 GAAATGAGTGGGAAAGAGAGCATCAAGAGAGAGAGCCAGATGAGACTGAAGACATCAAG 1620
Qy 4365 AAATAA 4370
Db 1621 AAATAA 1626

RESULT 14
AAS33094
ID AAS33094 standard; cdNA; 1455 BP.

AC AAS33094;

XX
DT 04-DEC-2001 (first entry)

XX DNA encoding human secreted protein, Seq ID No 53.

XX Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina;
KW rheumatoid arthritis; antiarteriosclerotic; cardiac; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmological;
KW cytostatic; Alzheimer's disease; Parkinson's disease; human; cancer;
KW multiple sclerosis; cancer; hyperproliferative disorder; infection;
KW Gaucher's disease; neurological disease; cerebrovascular disorder;
XX thrombosis; wound healing; ss.

XX Homo sapiens.

OS
PN WO200155326-A2.

XX
PD 02-AUG-2001.

XX
PF 17-JAN-2001; 2001WO-US001347.

XX
PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0241826P.
PR 08-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0244647P.
PR 08-NOV-2000; 2000US-02446475P.
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PR 08-NOV-2000; 2000US-0245282P.
PR 08-NOV-2000; 2000US-0245323P.
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PR 08-NOV-2000; 2000US-0246610P.
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PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.

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PR 17-NOV-2000; 2000US-0249212P.
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PR 17-NOV-2000; 2000US-0249214P.
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PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-451931/48.
DR P-PSDB; AAU20385.
DR
XX
PT New nucleic acids and polypeptides, useful for diagnosing, preventing or
PT treating medical conditions.
XX
XX Claim 1; SEQ ID NO 53; 753pp; English.
XX
CC The invention relates to novel isolated nucleic acid molecules (I)
CC encoding human secreted proteins (II). (I) and (II) are used to prevent,
CC treat or ameliorate a medical condition in e.g. humans, mice, rabbits,
CC goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in
CC the prevention, treatment and diagnosis of diseases associated with
CC inappropriate expression of secreted proteins. (I) and complementary
CC sequences may also be used as DNA probes in diagnostic assays (e.g.
CC polymerase chain reactions (PCR)) to detect and quantitate the presence
CC of similar nucleic acid sequences in samples, and so which patients may
CC be in need of restorative therapy. (II) may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of the secreted
CC proteins. The anti-(II) antibodies and antagonists may also be used to
CC down regulate expression and activity of (II). The anti-(II) antibodies
CC may also be used as diagnostic agents for detecting the presence of (II)
CC in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The
CC disorders include for example: immune/autoimmune diseases (e.g. HIV
CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
CC Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
CC cerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and
CC thrombosis), infections caused by bacteria, viruses and fungi and ocular
CC disorders (e.g. corneal infections). (I) and (II), agonists, antagonists
CC and antibodies can also be used to promote wound healing, maintain organs
CC before transplantation, and support cell culture of primary tissues.
XX
XX Query Match 30.2%; Score 1439.8; DB 4; Length 1455;

Best Local Similarity 99.5%; Pred. No. 0;
Matches 1441; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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QY 3294 GAACTGGATCCATTATGCTGTATGCTCAGGGGCTGACCTTTGTAGAGATCGGACCTT 3353
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DB 302 CTTATTGAAACTTCTCCAGTTCTACAAAATTTACTGAGTTTGAAGAAAGCAATTTGAGTA 361
QY 3594 ATTTTACTCATGTTTCGACTTTGCGCAAGGGCAATTCATTTGAGAACTGTGGGATTTAAC 3653
DB 362 ATTTTACTCATGTTTCGACTTTGCGCAAGGGCAATTCATTTGAGAACTGTGGGATTTAAC 421
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XX AAS34779;				PR	01-SEP-2000;	2000US-0229343P.
AC AAS34779;				PR	01-SEP-2000;	2000US-0229344P.
XX 04-DEC-2001 (first entry)				PR	01-SEP-2000;	2000US-0229345P.
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KW muscular disorder; reproductive disorder; gastrointestinal disorder;				PR	06-SEP-2000;	2000US-0230438P.
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XX Homo sapiens.				PR	08-SEP-2000;	2000US-0232081P.
XX WO20015163-A1.				PR	12-SEP-2000;	2000US-0231968P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX P-PSDB; AAU21580.
XX WPI; 2001-465558/50.
XX P-PSDB; AAU21580.
XX Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, and for treating cancers, rheumatoid arthritis.
XX
PS Claim 4; SEQ ID NO 23; 687pp; English.
XX
XX The present invention relates to the isolation of novel human neoplastic
CC disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA
CC sequences encoding for these polypeptides. The sequences of the invention
CC are useful in the diagnosis, treatment, prevention and/or prognosis of
CC disorders involving neoplastic disease such as hyperproliferative
CC disorders (e.g. leukemia, bone cancer, bladder cancer, brain stem
CC glioma, adult liver cancer, childhood cerebellar astrocytoma, or
CC Hodgkin's lymphoma). The sequences of the invention may also be useful
CC for treating other disorders such as neural disorders, immune system
CC disorders, pulmonary disorders, reproductive disorders, gastrointestinal
CC disorders, muscular disorders, cardiovascular disorders and renal
CC disorders. The polynucleotide sequences of the invention are also useful
CC in gene therapy. AAS34767-AAS35050 represent cDNA sequences encoding for
CC the novel human neoplastic disease associated polypeptides of the

CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1458 BP; 447 A; 291 C; 334 G; 386 T; 0 U; 0 Other;
Query Match 29.4%; Score 1398.6; DB 4; Length 1458;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1412; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2005, 14:31:04 : Search time 17358 Seconds
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Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

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Listing first 45 summaries

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9: gb_gss1.*
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11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1520.4	31.9	3271	4	AK077549 Mus muscu
3	1496.2	31.4	1920	11	DQ052679 Pan trogl
4	1057.2	22.2	1433	10	AY411000 Homo sapi
5	994.8	20.9	1439	10	AY411001 Pan trogl
6	934.8	19.6	1094	7	CR753926 CR753926
7	899.2	18.9	1081	7	CR755186 CR755186
8	851.4	17.9	904	5	BQ883603 AGENCOURT
9	818.8	17.2	896	1	AU120566 AU120566
10	797.6	16.7	826	7	CR977645 CR977645
11	793.8	16.7	867	1	AU142521 AU142521
12	793.2	16.6	1436	10	AY411002 Mus muscu
13	763.2	16.0	826	6	CA454899 AGENCOURT
14	755.8	15.9	888	5	BUI55281 AGENCOURT
15	752.6	15.8	794	3	BI753613 603028687
16	741.2	15.6	783	2	BI255087 602975932
17	738	15.5	915	2	BE798610 601581671
18	732.2	15.4	739	8	DR423059 nav20h04
19	719.4	15.1	940	7	CR981843 CR981843
20	716.8	15.0	803	2	BI253637 602975314
21	714.8	15.0	718	6	CF129160 UI-HF-ES0
22	712.4	15.0	836	5	BU053284 UI-M-FC0-

23	699.2	14.7	937	5	BQ891765 AGENCOURT
24	693.6	14.6	902	5	BUI62344 AGENCOURT
25	690	14.5	913	5	BQ900202 AGENCOURT
26	682	14.3	822	8	CK205797 MNS09546
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27	678.2	14.2	710	5	BUI619068 UI-H-FH1-
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35	654.8	13.7	728	2	BG031673 602300826
36	654.4	13.7	794	7	CN531342 UI-M-HQ0-
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38	646.8	13.6	875	6	CF108304 Shultzomi
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40	641.4	13.5	813	7	CN528777 UI-M-HQ0-
41	637.8	13.4	713	7	CK833369 4057248 B
42	637	13.4	787	2	BE545843 601071744
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44	633.6	13.3	943	5	BQ959595 AGENCOURT
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ALIGNMENTS

RESULT 1
LOCUS DQ052678 1920 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens RNASE3L gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ052678
VERSION DQ052678.1 GI:66898625
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1920)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1920)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
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Best Local Similarity 89.1%; Pred. No. 0;
Matches 1768; Conservative 0; Mismatches 123; Indels 93; Gaps 1;

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Db	1	ATGTCGCTCCACCCGGGACGAGGGGTCTCCCGAGGACGAGGAGCAATGGAGCCAGACCC	60	Db	988	GRCCGTTGGAGTGACAAACGAGAGTTCTGGCAAGACAAAGAACTATACCTCAATCAAGGAA	1047
QY	333	TCAGCACCAATCTCTTTAGGCCCCAAAATCTGAGGCTGCTTCAACCTCAGCAGGCTCTGTG	392	QY	1413	AAAGAGCCCGAGGAGACCAATGCTCGACAAAGATGAGGAGGAAAGAGAACTTCTTAAG	1472
Db	61	TCAGCACCAATCTCTTTAGGCCCCAAAATCTGAGGCTGCTTCAACCTCAGCAGGCTCTGTG	120	Db	1048	AAAGAGCCCGAGGAGACCAATGCTCGACAAAGATGAGGAGGAAAGAGAACTTCTTAAG	1107
QY	393	CAATATCAATATGAACTCCAGTGCCTTCCACCACTTCTCAAACTCTCCAGGCCCC	452	QY	1473	CTGTGTGATTCGATGCACTCATTCAGAAAACCTACTCTCCAGTGACCCCATGGATCAG	1532
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QY	513	CAAGGCGCTCTTCCCGCTGSCCAATCAGGCGCGCTTTCCCAACCAACAGATGAGGAC	572	QY	1593	GAGGAGTTGGGGAGGAGGCAAGAAAGGCAAGCTGCTCGGCTCCGTGGGAACTCCA	1652
Db	241	CAAGGCGCTCTTCCCGCTGSCCAATCAGGCGCGCTTTCCCAACCAACAGATGAGGAC	300	Db	1228	GAGGAGTTGGGGAGGAGGCAAGAAAGGCAAGCTGCTCGGCTCCGTGGGAACTCCA	1287
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Db	301	NN	360	Db	1288	AAGACCAAGCTCGATGAAGATTTAGAGAGTTCCAGTGAATCCGAGTGTGATGTAG	1347
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Db	361	NN	420	Db	1348	GACAGCACCTGTTCTAGCAGCTCAGACTCTGAAGTTTGTGACGTTATTGACAGAAATCAAA	1407
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Db	421	TCATGCTCATCCCCCGCCCCCTCCAGTATGCGCAGCAGGTTAATATCAGTACCT	480	Db	1408	CGCAAAAGGCCCCACCTGACCCACTTCATGATGAATTTGGTACAAACGATCCAGGCCAG	1467
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Db	541	AGTTCTTTCTGCGCCAGTGCTAATAACAGCAGTATGCTCTCAATTCAGACATCTCCCTCCA	600	Db	1528	AGCATTTATCTCGAGAGAGGCCATCAAGCCCTGCTGCTCTATGACCAACATGCTGGC	1587
QY	873	TACCACTCTCCAAAGGCTCCAGTGAGAGAGGTCCCAAGAAAGGCTGAAACATATGAT	932	QY	1953	AGACTTTTCCACTACCGGATCAGAGTCTCCCGCCTACGAACTTTTAACTGACAGGCCA	2012
Db	601	TACCACTCTCCAAAGGCTCCAGTGAGAGAGGTCCCAAGAAAGGCTGAAACATATGAT	660	Db	1588	AGACTTTTCCACTACCGGATCAGAGTCTCCCGCCTACGAACTTTTAACTGACAGGCCA	1647
QY	933	GACACAGGCAACGAGACCAAGTATGAGGAGGAGTCCGCTCCCTGATCGG	992	QY	2013	ACTGTTATGAATACGATGATACGAGTATATCTTTGAAAGGATTTCTATGTTTGCACAT	2072
Db	661	GACACAGGCAACGAGATCAAGTATGAGGAGGAGTCCGCTCCCTGATCGG	720	Db	1648	ACTGTTATGAATACGATGATACGAGTATATCTTTGAAAGGATTTCTATGTTTGCACAT	1707
QY	993	CGGAGCGAGGCGCGAGTCCGACAGGAGAGAGCAAGACAGCGGATCTGATTTAT	1052	QY	2073	GCCCCCTGACCAATATTTCCACTGCTGTAAGTAAATAGATTCAACATAGACTACCGATT	2132
Db	721	CGGAGCGAGGCGCGAGTCCGACAGGAGAGAGCAAGACAGCGGATCTGATTTAT	780	Db	1708	GCCCCCTGACCAATATTTCCACTGCTGTAAGTAAATAGATTCAACATAGACTACCGATT	1767
QY	1053	GACGAGGAGGAGAACCACTCTCGCACCGCAGCTACGAAACGAGCAGAGCGGAGACGG	1112	QY	2133	CATTTTATGAAGAGATGATGCGCGAGAAATTTTGTGAAAGGGCTTGAACCTTTTCA	2192
Db	781	GACGAGGAGGAGAACCACTCTCGCACCGCAGCTACGAAACGAGCAGAGCGGAGACGG	840	Db	1768	CATTTTATGAAGAGATGATGCGCGAGAAATTTTGTGTAAGGGCTTGAACCTTTTCA	1827
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RESULT 2
AK077549
LOCUS
DEFINITION
Mus musculus 8 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:5730445E20 product:weakly similar to
RIBONUCLEASE III (EC 3.1.26.3) (RNASE III) (P241) (Homo sapiens),
full insert sequence.
ACCESSION
AK077549

3271 bp mRNA linear HTC 03-APR-2004

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VERSION      AK077549.1  GI:26097404
KEYWORDS     HTC; CAP trapper.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    Bukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
JOURNAL      Sciurognathi; Muridae; Murinae; Mus.
PUBLISHED   1
TITLE        Carninci, P. and Hayashizaki, Y.
PUBMED      10349636
REFERENCE    2
AUTHORS      High-efficiency full-length cDNA cloning
TITLE        Meth. Enzymol. 303, 19-44 (1999)
JOURNAL     10349636
PUBLISHED   2
REFERENCE    3
AUTHORS      Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
TITLE        Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL     11042159
PUBLISHED   3
REFERENCE    4
AUTHORS      Normalization and subtraction of cap-trapper-selected cDNAs to
TITLE        prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
PUBLISHED   11042159
REFERENCE    5
AUTHORS      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
TITLE        Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
JOURNAL     Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
PUBLISHED   Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
REFERENCE    Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
AUTHORS      Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
TITLE        Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
JOURNAL     RIKEN integrated sequence analysis (RISA) system--384-format
PUBLISHED   sequencing pipeline with 384 multicapillary sequencer
REFERENCE    Genome Res. 10 (11), 1757-1771 (2000)
AUTHORS      11076861
TITLE        4
JOURNAL     The RIKEN Genome Exploration Research Group Phase II Team and the
PUBLISHED   FANTOM Consortium.
REFERENCE    Functional annotation of a full-length mouse cDNA collection
AUTHORS      Nature 409, 685-690 (2001)
TITLE        5
JOURNAL     The FANTOM Consortium and the RIKEN Genome Exploration Research
PUBLISHED   Group Phase I & II Team.
REFERENCE    Analysis of the mouse transcriptome based on functional annotation
AUTHORS      of 60,770 full-length cDNAs
TITLE        Nature 420, 563-573 (2002)
JOURNAL     6 (bases 1 to 3271)
PUBLISHED   Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
REFERENCE    Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
AUTHORS      Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hirozane, T.,
TITLE        Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
JOURNAL     Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
PUBLISHED   Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
REFERENCE    Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
AUTHORS      Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
TITLE        Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
JOURNAL     Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S.,
PUBLISHED   Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
REFERENCE    Muramatsu, M. and Hayashizaki, Y.
AUTHORS      Direct Submission
TITLE        Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
JOURNAL     Physical and Chemical Research (RIKEN), Laboratory for Genome
PUBLISHED   Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
REFERENCE    RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
AUTHORS      Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp,
TITLE        URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
JOURNAL     Fax: 81-45-503-9216]
PUBLISHED   cDNA library was prepared and sequenced in Mouse Genome
REFERENCE    Encyclopedia Project of Genome Exploration Research Group in Riken
AUTHORS      Genomic Sciences Center and Genome Science Laboratory in RIKEN
TITLE        Division of Experimental Animal Research in Riken contributed to
JOURNAL     prepare mouse tissues.
PUBLISHED   please visit our web site for further details.
REFERENCE    URL: http://genome.gsc.riken.jp/
AUTHORS      URL: http://fantom.gsc.riken.jp/.
TITLE        Location/Qualifiers
JOURNAL     1. 3271
PUBLISHED   1945
REFERENCE    1945
FEATURES     source

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Qy 1347 GAAAAAGACCGTTGGAGTGACCAACAGAGTCTTGGCAAGACAGAACTATACCTCAATC 1406
Db 181 GAAAAAGACAGATGGAGCGCAGCCAGGGCTCTGGCAAGAGAGAGAACTACACGTCATC 240

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Db 361 GGATCAGGTGGAGACTCGACTGTGTGAGGACAAAGCAGGCTCCGTGATTTGTATGACAA 420

Qy 1586 ATTTGAGGAGAGTTGGGGAGCAGGCAAGAAAGCCAAAGCTCTCGGCTCCGTGGGA 1645
Db 421 ATTTGAGGAGAAATTTGGGGAATAGGCAAGAGAGAGCCAAAGCTCCCGGCTCCGTGGGA 480

Qy 1646 ACCTCCAAAGACGAAGCTCGATGAAGATTTAGAGAGTTCCAGTGAATCCGAGTGTGAGTC 1705
Db 481 GCCTCCGAAGACAAAGCTGGATGAAGATTTAGAGAGTTCCAGTGAATCCGAGTGTGAGAC 540

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Qy 1766 AATCAACGCAAAAGAGCCCAACCTGACCGACTTCATGATGAACCTTTGGTACAACGATCC 1825
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Db 661 AGCCAGATGACGATGAGACCGCTTTCGAAAAATGCAAGAGCCGACGACAGGAA 720

Qy 1885 TTAGGCAACAGATTATTCCTGGAGAGAGGCGCATCAAGCCCTGTGCTCTATGACCAACA 1944
Db 721 TCCGCCACAGCATTTATCCCGGAGAGAGGCGCATCAAGCCCTGTGCTCTATGACCAACA 780

Qy 1945 ATGCTGGCAGACTTTTCCACTACCGGATCAGCTCTCCCGCCTACGACTTTTAACTG 2004

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Qy	2305	GATTTCTTCAGATGGAGGAAGGAGTCTGCTCCATGCGACCCAGATTTCTCTGACTTGT	2364
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TITLE			
JOURNAL			
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GENOMIC SURVEY SEQUENCE
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VERSION AY411000.1 GI:3976968
KEYWORDS GSS.
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ORGANISM Homo sapiens
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Hominidae; Homo.
REFERENCE 1 (bases 1 to 1443)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITILE Inferring nonneutral evolution from human-chimp-mouse orthologous
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gene trios
Science 302 (5652), 1960-1963 (2003)
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2 (bases 1 to 1443)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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VERSION AY411001.1 GI:39766969
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 1439)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios
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 2 (bases 1 to 1439)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
 Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, P., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 VERSION
 CR753926.1 GI:51865883
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 ORGANISM
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 REFERENCE
 CROS, N., Tkatchenko, A.V., Pisani, D.F., Leclerc, L., Leger, J.J.,
 MARINI, J.F. and Dechesne, C.A.
 Analysis of altered gene expression in rat soleus muscle atrophied
 by disuse
 J. Cell. Biochem. 83 (3), 508-519 (2001)
 11596118
 JOURNAL
 PUBMED
 COMMENT
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Lukyanov S, Cherkashin A, Moqadam P, Huang B, Lukyanov S, Campbell K, Gurskaya N, Svedberg ED, Sieber, PD. Suppression subtractive hybridization (SSH) method for generating differentially regulated or tissue specific cDNA probes and libraries. Proc Natl Acad Sci U S A. 1993; 93: 6025-30). Rats were female Sprague Dawley between 200 and 220g. Soleus muscle atrophy was performed by 14 days of hindlimb suspension."

ORIGIN

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Qy	2528	GTTCAACCCCGATGTGATTACTTTTCCGATATATCGTCCACTTTTGGGATACGCCCTGCACA	2587	
Db	660	GTTCAACCCCTGAAGTGATCACTTTCCGATATATCGTTCATCTTTGGGATACGCCCTGCACA	601	
Qy	2588	GTTGAGTTATGCAAGGAGACCAACAGTACCAAAAACCTGTGGAAGATTTATGTGAACCTTCG	2647	
Db	600	GTTGAGTTATGCAAGGAGACCCACAATACCAAAAATTTATGAAAAAGTTTACGTGAACCTTCG	541	
Qy	2648	CCACCTCTAGCAAAATAGTCCCAAGTCAACCAAACTGACAAACAGAGCTGGCCACAGAG	2707	
Db	540	CCACCTCTTAGCAAAATAGTCCCAAGGTCAACACAGACTGCAACAACAGAAAGCTGGCCAGAG	481	
Qy	2708	GGAGGAAGCCCTCCAAAAATACGGCAGAGAAATACAATCAGACGAGAAATTAACCGTGA	2767	
Db	480	GGAGGAAGCCCTCCAGBAGATACGGCAGAGAGACAAATCGCTCGAGAAATCACCGTGA	421	
Qy	2768	GCTAAGTAGCAAGGATCTTGGAAAACTGGGATCCGGTCTGTGATGTCTGTCAAGCATGCAAT	2827	
Db	420	GCTGAGTAGCAAGGATTTCTGGAAAACTGGCAATTCGTTCGTGATGTCTGTCAAGCATGCAAT	361	
Qy	2828	GATGCTACCTGTTCTGACCCATCATATCCGCTACCAACCAATGCTTAATGCATTTTGACAA	2887	
Db	360	GATGCTGCCTGTTCTGACCCATCATATCCGATACCAATGCTTAATGCATTTTGACAA	301	
Qy	2888	GTTGATAGGATATACTTTTCCAAGATCGTTGCTGTGTGACGTGGCCATGACTCATCCAAG	2947	
Db	300	GTTGATAGGATATACTTTTCAAGATCGTTGCTGTGTGACGTGGCCATGACTCATCCGAG	241	
Qy	2948	TCATCATTTTAAATTTTGGAAATGAATCTGTATCATGCAAGGAATTCATTAATCTAATGTGTG	3007	
Db	240	TCATCATTTTAAATTTTGGAAATGAATCTGTATCATGCAAGGAATTCCTGTCTAATGTGTG	181	

Qy	3008	AATTGGCAGCCCAATAACGAGACAGAAAAGTTTCATC	CATGCACATCGGGAAGNAAGG	3067
Db	180	AATTGGACAGCCCAATATGGAGACAGAAAGTTTCATC	CATGCACATCGGGAAGNAAGG	121
Qy	3068	GATTACACCTTGATAAATATCATGTCA	CGCTTGGCCAAGATGACCCCACTCCCTCGAG	3127
Db	120	AATTACACCCCTAATAATATCATGTCA	CGCTTCGGCCAAGATGCCA	61
Qy	3128	GATTACCAACAATGAACGGTTGGAAATCC	TGGTGGGTGATGCTGTTGTAATTTCTGCACAG	3187
Db	60	GATTATCAACAATGAAGGTTGAGATTCCT	GGGAGATGCTGTTGTCGATGTTCTGACCAAG	1

RESULT 8
 BQ883603
 LOCUS
 DEFINITION
 BQ883603
 5', mRNA sequence.
 ACCESSION
 BQ883603
 VERSION
 BQ883603.1
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.
 REFERENCE
 1 (bases 1 to 904)
 NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
 AUTHORS
 National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 Unpublished (1999)
 JOURNAL
 Contact: Robert Strausberg, Ph.D.
 COMMENT

REFERENCE	1 (bases 1 to 904)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: ARCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCW2537 row: p column: 11 High quality sequence spot: 695.

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FEATURES
source
1. .904
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6340858"
/tissue_type="neuroblastoma, cell line"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH MGC_47"
/note="Organ: Brain; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGACACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."

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	Query Match	17.9%;	Score 851.4;	DB 5;	Length 904;
	Best Local Similarity	97.8%;	Pred. No. 4.8e+209;		
	Matches 883;	Conservative 0;	Mismatches 18;	Indels 2;	Gaps 2;
QY	3480	CTCAATTATCTCTCCACCCACTCCAACTACAAAGAGCCAAATACTGATCGCAACTTATT			3539
DB	2	CTGGCTCAATTATCTCTCTCCCACTCCCACTACAAAGGCC-AAATACTGATCGCAACTTATT			60
QY	3540	GAACAATCTTCAGTTCCTACAAAACTTACTGTGATTTGAAGAGCAATTTGAGGTAAATTTTT			3599
DB	61	GAACAATCTTCAGTTCCTACAAAACTTACTGTGATTTGAAGAGCAATTTGAGGTAAATTTTT			120

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QY 3600 ACTCATGTTTCGACTTCTGGCAAGGCGATTCACATTCGAGAACTGTGGGATTTAAACCATCTG 3659
Db 121 ACTCATGTTTCGACTTCTGGCAAGGCGATTCACATTCGAGAACTGTGGGATTTAAACCATCTG 180
QY 3660 ACCCTAGGCCACAAATCAGAGAAATGGAATTCCTAGGTGACTCCATAATGCAACTGTGTAGCC 3719
Db 181 ACCCTAGGCCACAAATCAGAGAAATGGAATTCCTAGGTGACTCCATAATGCAACTGTGTAGCC 240
QY 3720 ACAGAGTACTTATTCATTCATTTCCAGATCATCATGAAGGACATTAACATTTGTTGGCA 3779
Db 241 ACAGAGTACTTATTCATTCATTTCCAGATCATCATGAAGGACATTAACATTTGTTGGCA 300
QY 3780 AGCTCTTTGGTGAATAATGAATCTAGGCCAAGGTAGCGAGAGCTGGCATGCAAGAG 3839
Db 301 AGCTCTTTGGTGAATAATGAATCTAGGCCAAGGTAGCGAGAGCTGGCATGCAAGAG 360
QY 3840 TAGCCATAACCAACGACAGACCAAGAGCCCTGTGCGCTTCGACCAAGACCTTTGGCG 3899
Db 361 TAGCCATAACCAACGACAGACCAAGAGCCCTGTGCGCTTCGACCAAGACCTTTGGCG 420
QY 3900 GACCTTTTGGAAATCATTTATTCAGGCGCTGTACACTGATAAGGATTTGGAATATGTTTCA 3959
Db 421 GACCTTTTGGAAATCATTTATTCAGGCGCTGTACACTGATAAGGATTTGGAATATGTTTCA 480
QY 3960 ACTTTCATGAATGTCGTCTTTTCCACGATTCGAAGAAATTCATTTTGAATCAGGATGG 4019
Db 481 ACTTTCATGAATGTCGTCTTTTCCACGATTCGAAGAAATTCATTTTGAATCAGGATGG 540
QY 4020 AATGACCCCAATCCAGCTTCAGCAGTGTGCTTGACACTTAGGACAGAGCAAGAAAGAG 4079
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QY 4080 CCAGACATTCCTCTGTACAAGACTCTGCAGACAGTGGGCGCCATCCATGCGCCGAACCTAC 4139
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QY 4140 ACTGTGGCTGTTTATTTCAAGGGAGAAAGAAATAGGCTGTGGGAAAGCAAGATTTTCAG 4199
Db 661 ACTGTGGCTGTTTATTTCAAGGGAGAAAGAAATAGGCTGTGGGAAAGCAAGATTTTCAG 720
QY 4200 CAAGCGAAATGGAGCAGCAATGGATGCGCTTGCAAAAATATATTTTCCCGAGTGGCC 4259
Db 721 CAAGCGAAATGGAGCAGCAATGGATGCGCTTGCAAAAATATATTTTCCCGAGTGGCC 780
QY 4260 CATCAGAAGCGTTTCATCGAACGGAAGTACAGACAGAGTTTAAAGAAA-TGAGGTGGGA 4318
Db 781 CATCAGAAGCGTTTCATCGAACGGAAGTACAGACAGAGTTTANNAGAAATTTGAGTGGGA 840
QY 4319 AAGAGAGCATCAAGAGAGAGAGCCAGATGAGACTGAAGACATCAAGAAATAAAGGAGGC 4378
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QY 4379 ATG 4381
Db 901 ATG 903
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LOCUS AU120566 HEMBB1 Homo sapiens cDNA clone HEMBB1000947 5', mRNA
DEFINITION AU120566 896 bp mRNA linear EST 16-NOV-2004
sequence.
ACCESSION AU120566
VERSION AU120566.2 GI:55778916
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 896)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
```

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
HRI human cDNA project
Unpublished (2000)
On Oct 19, 2000 this sequence version replaced gi:10935801.
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3966
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBB1000947"
/cissue_type="whole embryo, mainly body"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBB1"
/note="Vector: pME18SFL3"

ORIGIN

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Query Match 17.2%; Score 818.8; DB 1; Length 896;  
Best Local Similarity 97.9%; Pred. No. 1.4e-200;  
Matches 882; Conservative 0; Mismatches 13; Indels 6; Gaps 5;  
QY 2052 GGATTTTCTATGTTGTCACATGCCCTCCCTGACCAATATTCACCTGTGTAAAGTAATTAGA 2111  
Db 1 GGATTTTCTATGTTGTCACATGCCCTCCCTGACCAATATTCACCTGTGTAAAGTAATTAGA 60  
QY 2112 TTCACATAGACTACACGATTCATTTCAITTAAGAGAGATGATGCCGAGAAATTTTGTGTG 2171  
Db 61 TTCACATAGACTACACGATTCATTTCAITTAAGAGAGATGATGCCGAGAAATTTTGTGTG 120  
QY 2172 AAAGGCTTGAACTCTTTTCACTGTTCCATTCAGAGATATTTTGGAAATTAATGATGG 2231  
Db 121 AAAGGCTTGAACTCTTTTCACTGTTCCATTCAGAGATATTTTGGAAATTAATGATGG 180  
QY 2232 AATCTTAAAGGCTCTTTGTTTGAAGCAGCCCTCCCTGCTGCCAAGATTTCAATTTTCATG 2291  
Db 181 AATCTTAAAGGCTCTTTGTTTGAAGCAGCCCTCCCTGCTGCCAAGATTTCAATTTTCATG 240  
QY 2292 CCAGGTTTCTTAAGATTTCTTCAGATGGAGGAAAGGAAGTGTCTGCTCCATGCCACAGATT 2351  
Db 241 CCAGGTTTCTTAAGATTTCTTCAGATGGAGGAAAGGAAGTGTCTGCTCCATGCCACAGATT 300  
QY 2352 CTCCTGTACTTGTTAAGGTCCAGCAAGCCCTGCTGCTGAGGAGGAGATGCCAATATG 2411  
Db 301 CTCCTGTACTTGTTAAGGTCCAGCAAGCCCTGCTGCTGAGGAGGAGATGCCAATATG 360  
QY 2412 CTTTCAGTGGGAGGAGCTGGAGTGGCAGAAATATGCAGAAGATGCAGAGGCATGATTTGTT 2471  
Db 361 CTTTCAGTGGGAGGAGCTGGAGTGGCAGAAATATGCAGAAGATGCAGAGGCATGATTTGTT 420  
QY 2472 ACCAACCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2531  
Db 421 ACCAACCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
QY 2532 AACCCCGATGTGATTAATTTTCCGATTTATCGTCCATTTTGGGATACGCGCTGCGACAGTTG 2591  
Db 481 AACCCCGATGTGATTAATTTTCCGATTTATCGTCCATTTTGGGATACGCGCTGCGACAGTTG 540  
QY 2592 AGTTATGAGAGAGACCCACAGTACAAAACCTGTGGAGAGTATGTGAACTTCGCCAC 2651  
Db 541 AGTTATGAGAGAGACCCACAGTACAAAACCTGTGGAGAGTATGTGAACTTCGCCAC 600  
QY 2652 CTCCTAGCAATATGTCCTCCAAAGTCAAACTGACAAACAGAAAGCTGGCACAGAGGAG 2711
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Db      601  CTCTAGCAATAGTCCCAAGTCAACAACTGACAAACGAGAGCTGGACAGAGGAG 660
Qy      2712 GAAGCCCTCCAAAATACGCGAGAGAAATCAATAGAGACGAGAGTAACGGTGGAGCTA 2771
Db      661  GAAGCCCTCCAAAATACGCGAGAGAAAT-CAATGAGACGAGAGTAACGGTGGAGCTA 719
Qy      2772 AGTAGCAAGGATTTCTGGAACCTGGCATCGTTCTGATGCTGTCAGCATGCAATGATG 2831
Db      720  AGTAGCAAGGATTTCTGGAACCTGGCATCGTTCTGATGCTGTCAGCATGCAATGATG 778
Qy      2832 CTACCTGTTCTGACCCATCATATCCGCTACCAATGCTTCAATGCAATTT-GGACAAAGTT 2890
Db      779  CT--CCTGTCTGACCCATCATATCG-ITCACCAATGCTTATGCAATTTGGGACAAAGTT 835
Qy      2891 GATAGGATATACCTTCCAAAGATCGTTCTGTTGTCAGCTGGCCATGATCACTCATCCAAAGTCA 2950
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Qy      2951 T 2951
Db      896 T 896

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RESULT 10
LOCUS   CR977645
DEFINITION CR977645 RZPD no.9016 Homo sapiens cDNA clone RZPDp901610941 5',
mRNA sequence.
ACCESSION CR977645
VERSION   CR977645.1 GI:68215973
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 826)
Heil,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D.
and Korn,B.
Human T-Lymphocytes library
Unpublished (2005)
Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; RZPDp901610941.
RZPDIIB; (Human T-Lymphocytes) RZPD LIB No.9016
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact:
Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de

```

This clone is available from RZPD;
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp901610941>
 contact RZPD (product-support@rzpd.de) for further information.
 Primer name: q3.4 . Primer sequence: CCGATAACAATTCACACAG.

FEATURES

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source      Location/Qualifiers
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
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                /tissue_type="T-Lymphocytes"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="RZPD no.9016"
                /notes="Vector: pQE80LSN_cloned; Site_1: SalI; Site_2:
                NotI; vector:
                http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml
                ; 1st strand cDNA was prepared from mRNA obtained from

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human T-Lymphocytes with a NotI - oligo(dT) primer [5'
 GACTAGTTAGATCGGACGGCCCTTTTCTTTTCTTTT 3'].
 Double-stranded cDNA was ligated to SalI adaptors,
 digested with NotI and cloned into the NotI and SalI sites
 of the pQE80LSN_cloned vector"

ORIGIN

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Query Match      16.7%; Score 797.6; DB 7; Length 826;
Best Local Similarity 99.4%; Pred. No. 4.3e-195;
Matches 811; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy      1305 CGCTCCCAAGTAGGAGAGAGAGAGAGCTCGTTGGGAGCAAGAAAAGACCGTTGAGT 1364
Db      1    CGTCTCCCAAGTAGGAGAGAGAGAGCTCGTTGGGAGCAAGAAAAGACCGTTGAGT 60
Qy      1365 GACAAACAGAGTTCTGCAAAAGCAAGAACTATACCTCAATCAAGGAAAAGACCCGAG 1424
Db      61  GACAAACAGAGTTCTGCAAAAGCAAGAACTATACCTCAATCAAGGAAAAGACCCGAG 120
Qy      1425 GAGACCATGCTGACAAAGATGAGGAGAGAGAGAACTTCTTAAGCCCTGTGTGATT 1484
Db      121  GAGACCATGCTGACAAAGATGAGGAGAGAGAACTTCTTAAGCCCTGTGTGATT 180
Qy      1485 CGATGCACTCATTTGAGAAAACCTACTCTCCAGTGACCCCATGATGATGAGTGGAGATTCT 1544
Db      181  CGATGCACTCATTTGAGAAAACCTACTCTCCAGTGACCCCATGATGATGAGTGGAGATTCT 240
Qy      1545 ACAGTGGTTGGAAACGAGTAGGCTTCGTGACTTATATGACAAATTTGAGGAGGAGTTGGGG 1604
Db      241  ACAGTGGTTGGAAACGAGTAGGCTTCGTGACTTATATGACAAATTTGAGGAGGAGTTGGGG 300
Qy      1605 AGCAGGCAAGAAAAGGCCAAAGCTGCTGGCCCTCGGTGGGAACTCCAAAGACGAGCTC 1664
Db      301  AGCAGGCAAGAAAAGGCCAAAGCTGCTGGCCCTCGGTGGGAACTCCAAAGACGAGCTC 360
Qy      1665 GATGAAGATTTAGAGAGTTCCAGTGAATCCAGTGAGTGTGAGTCTCATGAGGACAGCACCCTGT 1724
Db      361  GATGAAGATTTAGAGAGTTCCAGTGAATCCAGTGAGTGTGAGTCTCATGAGGACAGCACCCTGT 420
Qy      1725 TCTAGCAGCTCAGACTCTGAAAGTTTGTGAGCTTATTGCGAAATCAAAACGCAAAAGGCC 1784
Db      421  TCTAGCAGCTCAGACTCTGAAAGTTTGTGAGCTTATTGCGAAATCAAAACGCAAAAGGCC 480
Qy      1785 CACCTTGACGACTTCATGATGAATCTTTGTGTACAGATCCAGGCGAGATGATGATGGA 1844
Db      481  CACCTTGACGACTTCATGATGAATCTTTGTGTACAGATCCAGGCGAGATGATGATGGA 540
Qy      1845 CCACCTCTGCAAAATGCGAGCGCAAGGCAAGCGCACAGGAATTAGGCACAGCATTTATCCT 1904
Db      541  CCACCTCTGCAAAATGCGAGCGCAAGGCAAGCGCACAGGAATTAGGCACAGCATTTATCCT 600
Qy      1905 GGAGAAAGGCCCATCAAGCCCTGTCCTCTATGACCAACAATCTGTCGACAGACTTTTCCAC 1964
Db      601  GGAGAAAGGCCCATCAAGCCCTGTCCTCTATGACCAACAATCTGTCGACAGACTTTTCCAC 660
Qy      1965 TACCGGATCACAGTCTCCCGCTACGAACTTTTAACTGACAGGCCAACTGTTATAGAA 2024
Db      661  TACCGGATCACAGTCTCCCGCTACGAACTTTTAACTGACAGGCCAACTGTTATAGAA 720
Qy      2025 TACGATGATCACAGTATATCTTTGAAGGATTTCTATGTTTGCACATG-CCCCCTTGAC 2083
Db      721  TACGATGATCACAGTATATCTTTGAAGGATTTCTATGTTTGCACATGCCCCCTTGAC 780
Qy      2084 CAATATTCCCTGTGTAAAGTAATAGATTCAACAT 2119
Db      781  CAATATTCCCTGTGTAAAGTAATAGATTCAACCT 816

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RESULT 11
LOCUS   AU142521
DEFINITION AU142521 Y79A1 Homo sapiens cDNA clone Y79A1000458 5', mRNA
sequence.

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AU142521      867 bp      mRNA      linear      EST 05-AUG-2002
AU142521 Y79A1 Homo sapiens cDNA clone Y79A1000458 5', mRNA
sequence.

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Wed Dec 28 10:05:00 2005

ACCESSION	AU142521	GI:11004042	QY	3519	AATACTGATCGACAACTTTATTGAAACTTCTCCAGTTCTACAAAACTTACTGAGTTGAA	3578
VERSION	AU142521.1	GI:11004042	Db	481	ATACTGATCGACAACTTTATTGAAACTTCTCCAGTTCTACAAAACTTACTGAGTTGAA	540
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)		QY	3579	GAAGCAATGGAGTAATTTTACTCATGTTGCACTTCTGGCAAGGCGATTACATTGAGA	3638
ORGANISM	Homo sapiens		Db	541	GAAGCAATGGAGTAATTTTACTCATGTTGCACTTCTGGCAAGGCGATTACATTGAGA	600
REFERENCE	1 (bases 1 to 867)		QY	3639	ACTGTGGGATTAACCATCTGACCTAGCCCAATCAGAGAAATGGAATTCCTAGGTGAC	3698
AUTHORS	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.		Db	601	ACTGTGGGATTAACCATCTGACCTAGCCCAATCAGAGAAATGGAATTCCTAGGTGAC	659
TITLE	HRI human cDNA project		QY	3699	TCATAATGCAACTGGTAGCCACAGAGTACTTATTCAATTCCTAGATCATATGAA	3758
JOURNAL	Unpublished (2000)		Db	660	TCATAATGCAACTGGTAGCCACAGAGTACTTATTCAATTCCTAGATCATATGAA	719
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project: 5' - & 3' - end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.		QY	3759	GGACACTTAACCTTTGTTCGAAAGCTCTTGGTGAATATAGAACTCAGCCCAAGGTAGCG	3818
FEATURES	Location/Qualifiers		Db	720	GGACACTTAACCTTTGTTCGAAAGCTCTTGGTGAATATAGAACTCAGCCCAAGGTAGCG	778
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ORIGIN			Db	779	GGANGANTGGCATGCAGGAGTACGCCATAACCAACGACACCAAGAGGCTGTGGCG	835
Query Match	16.7%; Score 793.8; DB 1; Length 867;					
Best Local Similarity	96.6%; Pred. No. 4.3e-194;					
Matches	84; Conservative 0; Mismatches 25; Indels 5; Gaps 3;					
QY	3039	GTTCATCATGTCATCGCGAAGAAAGGATTAACACCTTGATATAATATCATGTACGC	3098			
Db	1	GTTCATCATGTCATCGCGAAGAAAGGATTAACACCTTGATATAATATCATGTACGC	60			
QY	3099	CTTGCCCAAGTATGCCAATCTCCCTCGAGGATTAACCAATGAACGTTGGATTCTGT	3158			
Db	61	CTTGCCCAAGTATGCCAATCTCCCTCGAGGATTAACCAATGAACGTTGGATTCTGT	120			
QY	3159	GGTATGCTGTGTGTAATTTCTGACACGCTCCATTTGTACTATTTGTTCTTAGTCTG	3218			
Db	121	GGTATGCTGTGTGTAATTTCTGACACGCTCCATTTGTACTATTTGTTCTTAGTCTG	180			
QY	3219	GAAGAAGGAGGATTAGCAACCTATCGGACTGCCATTTGTCAGATCAGACCTTGCCATG	3278			
Db	181	GAAGAAGGAGGATTAGCAACCTATCGGACTGCCATTTGTCAGATCAGACCTTGCCATG	240			
QY	3279	CTAGCAAGAAGAACTTGAACTGATCCATTTATGCTGTATGCTCAGCGGCTGACCTTGT	3338			
Db	241	CTAGCAAGAAGAACTTGAACTGATCCATTTATGCTGTATGCTCAGCGGCTGACCTTGT	300			
QY	3339	AGAGATCGGACCTTCGACATGCAATGGCCAAATGTTTTGAAGCTTTAATAGGAGCTGT	3398			
Db	301	AGAGATCGGACCTTCGACATGCAATGGCCAAATGTTTTGAAGCTTTAATAGGAGCTGT	360			
QY	3399	TACTTGGAGGGAAGCTCGGAGGAAGCCCAAGCAGTTATTGAGCGTTCCTCTTTAATGAT	3458			
Db	361	TACTTGGAGGGAAGCTCGGAGGAAGCCCAAGCAGTTATTGAGCGTTCCTCTTTAATGAT	420			
QY	3459	CCGACCTCGCGGAAGTCTGGCTCAATTTATCTCTCCACCTCCAACTCAAGAGCA	3518			
Db	421	CCGACCTCGCGGAAGTCTGGCTCAATTTATCTCTCCACCTCCAACTCAAGAGCA	480			
RESULT 12						
AY411002	1436 bp	DNA	linear	GSS 12-DEC-2003		
LOCUS	Mus musculus HCM4078 gene, VIRTUAL TRANSCRIPT, partial sequence,					
DEFINITION	genomic survey sequence.					
ACCESSION	AY411002					
VERSION	AY411002.1	GI:39766970				
KEYWORDS	GSS.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	1 (bases 1 to 1436)					
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios					
JOURNAL	Science 302 (5652), 1960-1963 (2003)					
PUBMED	14671302					
REFERENCE	2 (bases 1 to 1436)					
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
TITLE	Direct Submission					
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA					
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.					
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Best Local Similarity	60.0%; Pred. No. 7e-194;					
Matches	866; Conservative 0; Mismatches 570; Indels 7; Gaps 1;					

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RESULT 13

CA454899

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CA454899 826 bp mRNA linear EST 12-NOV-2002
AGENCOURT_10735747 MAPcL Homo sapiens cdna clone IMAGE:6722379 5',
mRNA sequence.

CA454899

CA454899.1 GI:24905082

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 826)

NIH-MGC <http://mgc.ncl.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Kristi A. Eglund, Ira Pastan

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence stop: 553.

Location/Qualifiers

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Directionally cloned. Priming method: oligo-dt. Average

insert size: 1800 bp. Library amplification: 26,000 fold.

Kristi A. Eglund, James J. Vincent, Robert Strausberg,

Bungkook Lee & Ira Pastan. Discovery of new breast

ORIGIN	cancer genes encoding membrane and secreted proteins. Manuscript submitted."									
	Query Match	16.0%;	Score	763.2;	DB	6;	Length	826;		
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	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. NIH-MGC http://mgs.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Scrausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTP cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Plate: LLAM13480 row: j column: 11 High quality sequence stop: 669. Location/Qualifiers 1. .888 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6148714" /tissue_type="melanotic melanoma" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 72" /notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2 kb. Library constructed by Life Technologies."									
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Qy      836 T 836
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VERSION BI753613.1 GI:15745191
KEYWORDS EST.
SOURCE  Homo sapiens (human)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE 1 (bases 1 to 794)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."

FEATURES
source

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Best Local Similarity 99.1%; Pred. No. 2.le-183;
Matches 788; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

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Job time : 17368 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	259.6	5.4	354	US-09-513-999C-8294	Sequence 8294, Ap
4	194.6	4.1	430	US-09-513-999C-11432	Sequence 11432, A
5	92	1.9	7218	US-08-232-463-14	Sequence 14, Appl
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7	62.8	1.3	726	US-09-107-532A-1780	Sequence 1780, Ap
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9	62.4	1.3	6251	US-08-956-171E-25	Sequence 25, Appl
10	62.4	1.3	6251	US-08-781-986A-25	Sequence 25, Appl
11	61.6	1.3	320	US-09-165-264-13	Sequence 13, Appl
12	61	1.3	699	US-09-583-110-1893	Sequence 1893, Ap
13	61	1.3	711	US-09-107-433-1791	Sequence 1791, Ap
14	60	1.3	687	US-09-543-681A-3474	Sequence 3474, Ap
15	59.8	1.3	320	US-09-165-264-11	Sequence 11, Appl
16	59.4	1.2	659	US-08-869-674-1	Sequence 1, Appli
17	59.4	1.2	699	US-09-213-010-1	Sequence 1, Appli
18	59.4	1.2	699	US-09-213-011-1	Sequence 1, Appli
19	59.4	1.2	1830121	US-09-557-884-1	Sequence 1, Appli
20	59.4	1.2	1830121	US-09-643-990A-1	Sequence 1, Appli
21	59.4	1.2	1830121	US-10-158-865-1	Sequence 8, Appli
22	59	1.2	319	US-09-165-264-8	Sequence 12, Appl
23	58	1.2	318	US-09-165-264-12	Sequence 126, App
24	57.8	1.2	13121	US-08-961-527-126	

ALIGNMENTS

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; Sequence 1, Application US/09900425B
; Patent No. 6737512
; GENERAL INFORMATION:
; APPLICANT: Wu, Hongjiang
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof
; FILE REFERENCE: IS15029/ISPH-0522
; CURRENT APPLICATION NUMBER: US/09/900, 425B
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 4764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-900-425B-1

Query Match 100.0%; Score 4764; DB 3; Length 4764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 11432
; LENGTH: 430
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 415
; OTHER INFORMATION: r=a or g
US-09-513-999C-11432

Query Match      4.1%; Score 194.6; DB 3; Length 430;
Best Local Similarity 96.7%; Pred. No. 9.9e-45;
Matches 208; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

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DB 277 CAACCCATATCATCAAGGAGCTGATATCTAGTGGAAAGATTAGACGCTGTGCATCTTCA 336
QY 178 CTATGATATGAGGAGCTCTGAGCTTATATCTCTGTGGAAGATGACATATCCAGGC 237
DB 337 CTATGATATGAGGAGCTCTGAGCTTATATCTCTGTGGAAGATGACATATCCAGGC 396
QY 238 GGAACATCATGATGCGAGGAAACACATGTCACAGA 272
DB 397 GGAACATCATGATGCA-GGAACACATGTCACAGA 430

RESULT 5
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109

; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

Query Match      1.9%; Score 92; DB 2; Length 7218;
Best Local Similarity 2.1%; Pred. No. 1.2e-14;
Matches 8; Conservative 258; Mismatches 118; Indels 0; Gaps 0;

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DB 1427 YYYYYYYYGTACCAATTTCTTA 1450

RESULT 6
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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
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[illegible]

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; TITLE OF INVENTION: NOVEL RUCS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,087
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dickinson, Todd Q
; REGISTRATION NUMBER: 28,354
; REFERENCE/DOCKET NUMBER: GM10116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2252
; TELEFAX: 215-994-2222
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 732 base pairs
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; STRANDEDNESS: double
; TOPOLOGY: linear
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; US-08-965-087-1
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; Query Match 1.3%; Score 62.8; DB 3; Length 732;
; Best Local Similarity 50.3%; Pred. No. 5.4e-07;
; Matches 154; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
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; QY 3433 TATTTTG 3438
; DB |||||
;
; DB 458 TTGCTG 463
;
; RESULT 9
; US-08-956-171E-25
; Sequence 25, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
;
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
;
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
;
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6251 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; US-08-956-171E-25
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; Query Match 1.3%; Score 62.4; DB 3; Length 6251;
; Best Local Similarity 50.0%; Pred. No. 3e-06;
; Matches 153; Conservative 1; Mismatches 152; Indels 0; Gaps 0;
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; QY 3133 ACCACATGACGGTTGGAATTCCTGGGTGATGCTGTGTGTAATTTCTGACGAGCGTCC 3192
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; QY 3193 ATTGTGACTATTGTTTCTAGTCTGGAAGAAGAGGATTTAGCAACCTATCGGACTGCCA 3252
; DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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; DB 5848 ATTTATTTGATAACATCCCACTTGCAGAGGGGAATTTAACAAAAATCGTGCCACTA 5907
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; QY 3253 TTGTTTCTGAGTACGACCTTTGCCATGCTAGCAAGAAAGAACTTGAACCTGGATCCATTTATGC 3312
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; QY 3313 TGTATGCTCAGGGCCCTGACCTTTGTAGAGAAATCGGACCTTCGACATGCAATGGCCAAAT 3372
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; QY 3373 GTTTTGAAGCGTTAATAGGAGCTGTTTACTTGGAGGGAAGCCCTGGAGGAAGCCAGCACT 3432
; DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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; DB 6028 CATTCGAAGCATTTATTGGGGCATTTGATTGGATCAAGGACTAGATATAGTTTGGAAAT 6087
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; QY 3433 TATTTTG 3438
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; DB 6088 TTGCTG 6093
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; RESULT 10

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RESULT 11
US-09-165-264-13/c
Application US/09165264

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	Best Local Similarity	48.0%	Pred. No. 3.3e-06			
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DB	28	CAGTTACAATAAATACTGGTTATCTTTTAAACAAACGAATTACTTTTACAGGCACATT	87			
QY	3111	GAACCAACTCCCTCGAGGATTAAACCAATGAACGGTTGGAAATTCCTGGGTGATGCTGTT	3170			
DB	88	ACTCACCGTAGTGCAAGTAGTAAACATAATGAACGGCTTAGAATTTTTAGTGATTTCAATT	147			
QY	3171	GTTGAATTTCTGACCAGCGTCCATTGTGTAATAATTTGTTTCTTAGTCTGGAGAGAGAGA	3230			
DB	148	CTAAGTTATGTCATTGCTTAATGGCTTTTACCACGCTTTCCCTTCGTGTCGATGAAGGGGAT	207			
QY	3231	TTAGCAACCTATCGGACTGCCATTGTTTCAAGATCAGACCTTTGCCATGCTAGCAAAAGAAA	3290			

us-10-774-974-1.rni

Wed Dec 28 10:04:59 2005

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QY      3351 CTTGACATGCAATGCGCAATGTTTGAAGCGTTAATAGGAGCTCTTTACTTGA 3406
Db      328 CGCGAATCTATTTGGCCGACACAGTAGAAGCGTTAATGTTGTTCTTTCTTGA 383

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RESULT 15
US-09-165-264-11/c
; Sequence 11, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamorthy, Thuraiayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-11

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Query Match      1.38; Score 59.8; DB 3; Length 320;
Best Local Similarity 49.8%; Pred. No. 2.2e-06;
Matches 151; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

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QY      476 CTTTGTACCTTTCCCGCCACCCATGCTCGTCAAGCAAGGCCCTTTCCCGCCCTGCCC 535
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QY      536 AATCAGGCGCGCTTTCCCAACACCAAGATGAGGCAACCCCTTCCAGTTCCCTTGT 595
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QY      716 TCC 718
Db      3 CCC 1

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Search completed: December 27, 2005, 03:24:37
Job time : 782 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2005, 15:11:52 ; Search time 3504 Seconds
(without alignments)
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Perfect score: 4764
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.Main:*

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- 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq.*
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- 9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4764	100.0	4764	5 US-10-079-185-1	Sequence 1, Appli
2	4764	100.0	4764	7 US-10-774-974-1	Sequence 1, Appli
3	4764	100.0	4764	10 US-11-001-993-1	Sequence 1, Appli
4	4760.8	99.9	4764	3 US-09-900-425A-1	Sequence 1, Appli
5	4760.8	99.9	4764	8 US-10-805-919-1	Sequence 1, Appli
6	4760.8	99.9	4764	8 US-10-723-860-280	Sequence 280, App
7	4760.8	99.9	4764	8 US-10-756-149-319	Sequence 319, App
8	4732.4	99.3	5425	8 US-10-723-860-5003	Sequence 5003, App
9	1619.6	34.0	1626	7 US-10-205-331-117	Sequence 117, App
10	1398.6	29.4	1458	5 US-10-103-313-23	Sequence 23, Appl
11	1262.4	26.5	1314	5 US-10-103-313-187	Sequence 187, App
12	770.2	16.2	4275	10 US-11-097-143-2408	Sequence 2408, Ap
13	703.8	14.8	6397	10 US-11-097-143-2407	Sequence 2407, Ap
14	518.2	10.9	578	9 US-10-779-543-6006	Sequence 6006, Ap
15	469.4	9.9	633	8 US-10-357-930-20941	Sequence 20941, A
16	469.4	9.9	633	8 US-10-357-930-20985	Sequence 20985, A
17	469.4	9.9	633	8 US-10-357-930-26789	Sequence 26789, A
18	469.4	9.9	633	8 US-10-357-930-26829	Sequence 26829, A
19	411.4	8.6	488	3 US-09-918-995-20306	Sequence 20306, A
20	405.4	8.5	583	3 US-09-814-353-19214	Sequence 19214, A
21	392.2	8.2	405	3 US-09-803-713-409	Sequence 409, App
22	392.2	8.2	405	9 US-10-779-543-13679	Sequence 13679, A
23	384	8.1	397	9 US-10-779-543-9312	Sequence 9312, Ap

ALIGNMENTS

RESULT 1

US-10-079-185-1
; Sequence 1, Application US/10079185
; Publication No. US20030044941A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof
; FILE REFERENCE: ISIS5030
; CURRENT APPLICATION NUMBER: US/10/079,185
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 09/479,783
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 08/870,608
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 08/659,440
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 09/900,425
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-185-1

Query Match 100.0%; Score 4764; DB 5; Length 4764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	AGCCTTTTATAGTTGCTTTTCCCGGGATGTGAAGGATACAGAAATGACTGTGAATCAA	120
Qy	121	CCCATATCATCAAGAGCTGATAAATCTAGTGAAGATTAGAGTTGATCTTCACTA	180
Db	121	CCCATATCATCAAGAGCTGATAAATCTAGTGAAGATTAGAGTTGATCTTCACTA	180
Qy	181	TGATATGAGGCAGTCTCTGAGCTTATATCTCTGTGGAGAGTGTGACATATCCAGCGGA	240
Db	181	TGATATGAGGCAGTCTCTGAGCTTATATCTCTGTGGAGAGTGTGACATATCCAGCGGA	240

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DB 241 ACATCATGATGAGGGAACACATGTCACAGATCTCGTTCCACCGGGAGAGGGCGTC 300
QY 301 CCCGAGGACGAGGAGACATGAGCCAGACCCTCAGCACCATCTCTTTAGGGCCCCAAAATC 360
DB 301 CCCGAGGACGAGGAGACATGAGCCAGACCCTCAGCACCATCTCTTTAGGGCCCCAAAATC 360
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DB 361 TGAGGCTGCTTCCACCTCAGACGCTCTCTGTGCAATATCAATATGAACTCCAAAGTGCC 420
QY 421 CTTTCAACAATCTTCAAACTCTCAGCCCCCAATTTCTCCTCCACGACGACTTTG 480
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Db 3421 AAGCCAAAGCAGTTATTTGAGCGTTGCTCTTTAATGATCCGACCTGCGCGAAGTCTGGC 3480
QY 3481 TCAATTTATCCTCCACCCCACTCAACTACAGAGCCAAATACTGATCGACAACTTATTTG 3540
Db 3481 TCAATTTATCCTCCACCCCACTCAACTACAGAGCCAAATACTGATCGACAACTTATTTG 3540

QY 3541 AAACTTCTCCAGTTCTCAAAAACTTACTGAGTTTGAAGAGCAATTCGAGTAATTTTTTA 3600
Db 3541 AAACTTCTCCAGTTCTCAAAAACTTACTGAGTTTGAAGAGCAATTCGAGTAATTTTTTA 3600
QY 3601 CTCAATGTTGAGTCTCTGGCAAGGCAATTCATTTGAGAACTGTGGGATTTAACCATCTGA 3660
Db 3601 CTCAATGTTGAGTCTCTGGCAAGGCAATTCATTTGAGAACTGTGGGATTTAACCATCTGA 3660
QY 3661 CCTTAGGCCCAATCAGAGAAATGGAAATTCCTAGGTGATCTCCATAATGCAACTGTGTAGCCA 3720
Db 3661 CCTTAGGCCCAATCAGAGAAATGGAAATTCCTAGGTGATCTCCATAATGCAACTGTGTAGCCA 3720
QY 3721 CAGAGTACTTATTTCATTTCCAGATCATCATGAAGGACACTTAACTTTGTTGGCAA 3780
Db 3721 CAGAGTACTTATTTCATTTCCAGATCATCATGAAGGACACTTAACTTTGTTGGCAA 3780
QY 3781 GCTCTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGGCATGCAAGAGT 3840
Db 3781 GCTCTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGGCATGCAAGAGT 3840
QY 3841 ACGCCATAACCAACGACCAAGAGGCTGTGGCGCTTCGACCAAGACCTTGGCGG 3900
Db 3841 ACGCCATAACCAACGACCAAGAGGCTGTGGCGCTTCGACCAAGACCTTGGCGG 3900
QY 3901 ACCTTTTGGAAATCATTTATTGTCAGCGCTGTACACTGTATAAGGATTTGGAAATATGTTTCATA 3960
Db 3901 ACCTTTTGGAAATCATTTATTGTCAGCGCTGTACACTGTATAAGGATTTGGAAATATGTTTCATA 3960
QY 3961 CTTTTCATGAATGTCGTTCTTTCCAGATGTAAGAAATTCATTTTGAATCAGGATTTGGA 4020
Db 3961 CTTTTCATGAATGTCGTTCTTTCCAGATGTAAGAAATTCATTTTGAATCAGGATTTGGA 4020
QY 4021 ATGACCCCAAAATCCAGCTTCAGCAGTGTGCTTGACACTTTAGGACAGAGGAAAAGAGC 4080
Db 4021 ATGACCCCAAAATCCAGCTTCAGCAGTGTGCTTGACACTTTAGGACAGAGGAAAAGAGC 4080
QY 4081 CAGACATTCCTCTGTACAAGACTCTGCAGACAGTGGGCCCATGCCATGCCCAACCTTACA 4140
Db 4081 CAGACATTCCTCTGTACAAGACTCTGCAGACAGTGGGCCCATGCCATGCCCAACCTTACA 4140
QY 4141 CTGTGCTGTTTATTTCAGGGGAGAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTTCAGC 4200
Db 4141 CTGTGCTGTTTATTTCAGGGGAGAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTTCAGC 4200
QY 4201 AAGCGAAATGGGAGCAGCAATGGATGCCCTTGAAATAATATTTTCCCAAGATGGCCC 4260
Db 4201 AAGCGAAATGGGAGCAGCAATGGATGCCCTTGAAATAATATTTTCCCAAGATGGCCC 4260
QY 4261 ATCAGAAGCGGTTTCATCGAAACGGAAGTACAGACAGAGTTTAAAGAAATGAGGTGGGAAA 4320
Db 4261 ATCAGAAGCGGTTTCATCGAAACGGAAGTACAGACAGAGTTTAAAGAAATGAGGTGGGAAA 4320
QY 4321 GAGAGCATCAAGAGAGAGCCAGATGAGACTGAAGACATCAAGAAATAAAGAGGAGGCAT 4380
Db 4321 GAGAGCATCAAGAGAGAGCCAGATGAGACTGAAGACATCAAGAAATAAAGAGGAGGCAT 4380
QY 4381 GCAAGTGTGGATTTTACTGCTCAGTAACTGTGACTGTTGCTTATTGAGACCTAGCCT 4440
Db 4381 GCAAGTGTGGATTTTACTGCTCAGTAACTGTGACTGTTGCTTATTGAGACCTAGCCT 4440
QY 4441 AGTTTTTCTGTCAGACAATGAACGAAGTGTGCTCATTTGAAATAAAATACAGAGTCAAAATCG 4500
Db 4441 AGTTTTTCTGTCAGACAATGAACGAAGTGTGCTCATTTGAAATAAAATACAGAGTCAAAATCG 4500
QY 4501 CTATTGTTGTTTTAATGATCTGTTTTAGCTGGAATGCTTTTATTAACAAAGTATTAGATT 4560
Db 4501 CTATTGTTGTTTTAATGATCTGTTTTAGCTGGAATGCTTTTATTAACAAAGTATTAGATT 4560
QY 4561 TTTCTTCTATTAAACGGAAAACCTTGACTTTGTTGTAATGTGCATTTACTTCTTTTATTTTG 4620
Db 4561 TTTCTTCTATTAAACGGAAAACCTTGACTTTGTTGTAATGTGCATTTACTTCTTTTATTTTG 4620

QY 1621 CCAAAGCTGCTCGSCCTCCGTGGGAACCTCCAAAGACGAAGCTCGATGAAGATTTCAGGA 1680
DB 1621 CCAAAGCTGCTCGSCCTCCGTGGGAACCTCCAAAGACGAAGCTCGATGAAGATTTCAGGA 1680
QY 1681 GTTCCAGTGAATCCGAGTGTGAGTCTGATGAGGACAGCACCTGTTCTTAGCAGCTCAGACT 1740
DB 1681 GTTCCAGTGAATCCGAGTGTGAGTCTGATGAGGACAGCACCTGTTCTTAGCAGCTCAGACT 1740
QY 1741 CTGAAGTTTTGAGCTTTATTCAGAAATCAACGCAAAAAGGCCACCCTGACCGACTTC 1800
DB 1741 CTGAAGTTTTGAGCTTTATTCAGAAATCAACGCAAAAAGGCCACCCTGACCGACTTC 1800
QY 1801 ATGATGAACCTTTGTGTAACACGATCCAGGCCAGATGAATGATGACCACTCTGCAAAATGCA 1860
DB 1801 ATGATGAACCTTTGTGTAACACGATCCAGGCCAGATGAATGATGACCACTCTGCAAAATGCA 1860
QY 1861 GCGCAAGGCAAGACGCAAGGAATTAGGCAAGCACTTTATCTCTGGAGAGAGGCCATCA 1920
DB 1861 GCGCAAGGCAAGACGCAAGGAATTAGGCAAGCACTTTATCTCTGGAGAGAGGCCATCA 1920
QY 1921 AGCCCTGTCTCTATGACCAACAAATGCTGGGAGACTTTTCCACTACCGGATCACAGTCT 1980
DB 1921 AGCCCTGTCTCTATGACCAACAAATGCTGGGAGACTTTTCCACTACCGGATCACAGTCT 1980
QY 1981 CCCGGCTACGAACCTTTTAACTGACAGGCCAACTGTTATAGAAATACGATGATCAGAGT 2040
DB 1981 CCCGGCTACGAACCTTTTAACTGACAGGCCAACTGTTATAGAAATACGATGATCAGAGT 2040
QY 2041 ATATCTTTGAAGGATTTCTATGTTTGCAATGCCCCCTCGACCAATATTCCTCTGTGTA 2100
DB 2041 ATATCTTTGAAGGATTTCTATGTTTGCAATGCCCCCTCGACCAATATTCCTCTGTGTA 2100
QY 2101 AGTAATATAGATTCACATAGACTACACGATTCATTTCAATGTAAGAGATGATCCGGAGA 2160
DB 2101 AGTAATATAGATTCACATAGACTACACGATTCATTTCAATGTAAGAGATGATCCGGAGA 2160
QY 2161 ATTTTGTGTGAAGGCTTGAACCTTTTCACTGTTCTTCACTGTTCTTCACTGATATTTTGGAT 2220
DB 2161 ATTTTGTGTGAAGGCTTGAACCTTTTCACTGTTCTTCACTGTTCTTCACTGATATTTTGGAT 2220
QY 2221 TATATGACTGGAATCTTTAAAGTCTCTTTGTTGAAGACAGCCCTCCCTGCTGCCCAAGAT 2280
DB 2221 TATATGACTGGAATCTTTAAAGTCTCTTTGTTGAAGACAGCCCTCCCTGCTGCCCAAGAT 2280
QY 2281 TTCAATTCATGCCACGTTTGTGAAGATTTCTCCAGATGAGGAAAGAGTCTGTCCA 2340
DB 2281 TTCAATTCATGCCACGTTTGTGAAGATTTCTCCAGATGAGGAAAGAGTCTGTCCA 2340
QY 2341 TGCACCAAGATTTCTCTGTACTTGTAAAGTGTGACAAAGCCCTGTTGCTTGAGGAGAGA 2400
DB 2341 TGCACCAAGATTTCTCTGTACTTGTAAAGTGTGACAAAGCCCTGTTGCTTGAGGAGAGA 2400
QY 2401 TTGCCAATATGCTTCAGTGGGAGAGCTGGAGTGGCAGAAATATGAGAAAGATGCAAG 2460
DB 2401 TTGCCAATATGCTTCAGTGGGAGAGCTGGAGTGGCAGAAATATGAGAAAGATGCAAG 2460
QY 2461 GCATGATTTGTACCAACCCCTGGGACGAAACCAAGCTCTGTCCGTATCGATCACTGGATC 2520
DB 2461 GCATGATTTGTACCAACCCCTGGGACGAAACCAAGCTCTGTCCGTATCGATCACTGGATC 2520
QY 2521 GTGAACAGTTTCAACCCCGATGTGATTAATTTTCCGATTAATCGTCCCACTTTGGGATACGCC 2580
DB 2521 GTGAACAGTTTCAACCCCGATGTGATTAATTTTCCGATTAATCGTCCCACTTTGGGATACGCC 2580
QY 2581 CTGCAGATTGATTTAGCAGGAGACCCACAGTACCAAAACTGTGGAAGATTATGTGA 2640
DB 2581 CTGCAGATTGATTTAGCAGGAGACCCACAGTACCAAAACTGTGGAAGATTATGTGA 2640
QY 2641 AACTTCGCCACCTCTTAGCAAAATAGTCCCAAGTCAAACAACTGACAAACAGAACTGG 2700
DB 2641 AACTTCGCCACCTCTTAGCAAAATAGTCCCAAGTCAAACAACTGACAAACAGAACTGG 2700
QY 2701 CACAGAGGGAGGAGCCCTCCAAAAAATACGGCAGAAAGATACAAATGAGACGGAAGTAA 2760

DB 2701 CACAGAGGGAGGAGCCCTCCAAAAAATACGGCAGAAAGATACAAATGAGACGGAAGTAA 2760
QY 2761 CGGTGGAGCTTAAGTAGCAAGGATTTCTGGAAAACTGGCATCCGTTCTGTCTGTCTGAGC 2820
DB 2761 CGGTGGAGCTTAAGTAGCAAGGATTTCTGGAAAACTGGCATCCGTTCTGTCTGTCTGAGC 2820
QY 2821 ATGCAATGATGCTACCTGTTCTGACCCCATCATATCCGCTACCAACATGCTTAATGATTT 2880
DB 2821 ATGCAATGATGCTACCTGTTCTGACCCCATCATATCCGCTACCAACATGCTTAATGATTT 2880
QY 2881 TGGACAAAGTTGATAGGATATACCTTTTCCAGATCGTTCTGTCTGTCTGAGCTGGCCATGACTC 2940
DB 2881 TGGACAAAGTTGATAGGATATACCTTTTCCAGATCGTTCTGTCTGTCTGAGCTGGCCATGACTC 2940
QY 2941 ATCCAAAGTCAATCAATTTAAATTTTGGAAATGAATCTGATCATGCGAGAAATTCATTACTA 3000
DB 2941 ATCCAAAGTCAATCAATTTAAATTTTGGAAATGAATCTGATCATGCGAGAAATTCATTACTA 3000
QY 3001 ACTGTGGAAATTCGGACGCCCAAAATACGGAGACAGAAAGTTTCATCATGACATGCGGA 3060
DB 3001 ACTGTGGAAATTCGGACGCCCAAAATACGGAGACAGAAAGTTTCATCATGACATGCGGA 3060
QY 3061 AGAAAGGATTAACACCTTGATAAATATCATGTACGCCCTTGGCCAGATGACCCAACTC 3120
DB 3061 AGAAAGGATTAACACCTTGATAAATATCATGTACGCCCTTGGCCAGATGACCCAACTC 3120
QY 3121 CCTCGAGGATTAACCAATGAAACGGTGGAAATTCCTGGGTGATGCTGTTGTTGAATTC 3180
DB 3121 CCTCGAGGATTAACCAATGAAACGGTGGAAATTCCTGGGTGATGCTGTTGTTGAATTC 3180
QY 3181 TGAACAGCTGCATTTGTGACTATTTGTTCTCTAGTCTGGAAGAGGAGATAGCAACCT 3240
DB 3181 TGAACAGCTGCATTTGTGACTATTTGTTCTCTAGTCTGGAAGAGGAGATAGCAACCT 3240
QY 3241 ATCGGACTGCATTTGTTGAGAACAGCACTCCCATGCTAGCAAGAAAGAACTTGAACCTGG 3300
DB 3241 ATCGGACTGCATTTGTTGAGAACAGCACTCCCATGCTAGCAAGAAAGAACTTGAACCTGG 3300
QY 3301 ATCCATTTATGCTGTATGCTCAGGSCCTGACCTTTTGTAGAGAAATCGGACCTTCGACATG 3360
DB 3301 ATCCATTTATGCTGTATGCTCAGGSCCTGACCTTTTGTAGAGAAATCGGACCTTCGACATG 3360
QY 3361 CAATGCCCAATTTGTTTGAAGCTTAATAGGAGCTGTTTACTTTGGAGGGAAGCTGAGG 3420
DB 3361 CAATGCCCAATTTGTTTGAAGCTTAATAGGAGCTGTTTACTTTGGAGGGAAGCTGAGG 3420
QY 3421 AAGCCAAAGCAGTTTATTTGGACGCTTCTTTTAAATGATCGGACCTGCGGAGTCTGGC 3480
DB 3421 AAGCCAAAGCAGTTTATTTGGACGCTTCTTTTAAATGATCGGACCTGCGGAGTCTGGC 3480
QY 3481 TCAATTTATCTCTCCACCCCACTCAAGAGCCAAATACTGATCGACAACTTTATTG 3540
DB 3481 TCAATTTATCTCTCCACCCCACTCAAGAGCCAAATACTGATCGACAACTTTATTG 3540
QY 3541 AAACTTCTCCAGTTCTACAAAACTTACTGAGTTTGAAGAGCAATGGAGTAATTTTA 3600
DB 3541 AAACTTCTCCAGTTCTACAAAACTTACTGAGTTTGAAGAGCAATGGAGTAATTTTA 3600
QY 3601 CTCATGTTTCGACTCTGGCAAGGGCAATTCACATTGAGAACTGTTGGATTTAAACATCTGA 3660
DB 3601 CTCATGTTTCGACTCTGGCAAGGGCAATTCACATTGAGAACTGTTGGATTTAAACATCTGA 3660
QY 3661 CCTTAGGCCCAATCAGAGAAATGGAATTCCTAGTGACTCCATAATGCAACTGTTAGCCA 3720
DB 3661 CCTTAGGCCCAATCAGAGAAATGGAATTCCTAGTGACTCCATAATGCAACTGTTAGCCA 3720
QY 3721 CAGAGTACTTATTCATTCTATTTCCAGATCATCATGAAGGACACTTAACTTTGTTGCGAA 3780
DB 3721 CAGAGTACTTATTCATTCTATTTCCAGATCATCATGAAGGACACTTAACTTTGTTGCGAA 3780
QY 3781 GCTCTTTGTGTAATATAGAACTCAGGCCAAGTAGCGGAGGAGCTGGGCACTCAGAGT 3840

; TITLE OF INVENTION: Human RNase III And Compositions And Uses Thereof									
; FILE REFERENCE: ISIS0003-104 (ISIS-5030US.D1)									
; CURRENT APPLICATION NUMBER: US/11/001,993									
; PRIOR FILING DATE: 2004-12-02									
; PRIOR APPLICATION NUMBER: 10/079,185									
; PRIOR FILING DATE: 2002-02-20									
; PRIOR APPLICATION NUMBER: 09/479,783									
; PRIOR FILING DATE: 2000-01-07									
; PRIOR APPLICATION NUMBER: 08/870,608									
; PRIOR FILING DATE: 1997-06-06									
; PRIOR APPLICATION NUMBER: 08/659,440									
; PRIOR FILING DATE: 1996-06-06									
; PRIOR APPLICATION NUMBER: 09/900,425									
; PRIOR FILING DATE: 2001-07-06									
; NUMBER OF SEQ ID NOS: 36									
; SOFTWARE: Patentin version 3.1									
; SEQ ID NO 1									
; LENGTH: 4764									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-11-001-993-1									
Query Match 100.0%; Score 4764; DB 10; Length 4764;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 4764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	CTGTCTTGTTAGTCTGCGGTAGTAGCTGGCTTTGCTCTGACGGCGATCTCGGGCCCGGAG	60						
DB	1	CTGTCTTGTTAGTCTGCGGTAGTAGCTGGCTTTGCTCTGACGGCGATCTCGGGCCCGGAG	60						
QY	61	AGCCTTTTATAGTCTCTTTCCGGGGATGTGAAGGATACAGAAATGACTGTGAATCAA	120						
DB	61	AGCCTTTTATAGTCTCTTTCCGGGGATGTGAAGGATACAGAAATGACTGTGAATCAA	120						
QY	121	CCCATATCATCAAGGAGCTGATAATCTAGTGGAAAGTGTAGAGTGTGCATATCTCACTA	180						
DB	121	CCCATATCATCAAGGAGCTGATAATCTAGTGGAAAGTGTAGAGTGTGCATATCTCACTA	180						
QY	181	TGATATGAGGAGCTCTGAGCTTATATCTCTGTGGAAGATGTGACATATCCAGGCGGA	240						
DB	181	TGATATGAGGAGCTCTGAGCTTATATCTCTGTGGAAGATGTGACATATCCAGGCGGA	240						
QY	241	ACATCATGATGACGGGAAACACATGTACAGAAATGTCTTCCACCCGGGACGAGGGCGTC	300						
DB	241	ACATCATGATGACGGGAAACACATGTACAGAAATGTCTTCCACCCGGGACGAGGGCGTC	300						
QY	301	CCCGAGACGAGGAGGACATGGAGCCGACCCCTCAGCACCATCTTTAGGCCCCCAAAATC	360						
DB	301	CCCGAGACGAGGAGGACATGGAGCCGACCCCTCAGCACCATCTTTAGGCCCCCAAAATC	360						
QY	361	TGAGGCTGTTTCAACCTCAGCAGCTCTGTGCAATATCAATATGAACCTTCCAAGTGCCC	420						
DB	361	TGAGGCTGTTTCAACCTCAGCAGCTCTGTGCAATATCAATATGAACCTTCCAAGTGCCC	420						
QY	421	CTTCCACCACTTTCTCAAACTCTCCAGCCGCCAATTTCTCCCTTCCACGACGACCTTG	480						
DB	421	CTTCCACCACTTTCTCAAACTCTCCAGCCGCCAATTTCTCCCTTCCACGACGACCTTG	480						
QY	481	TACCTTTCCGCCCAACCATGCTCCGTGAGCGAAGGCCCTTTTCCCTTCCCTTCCCAATCA	540						
DB	481	TACCTTTCCGCCCAACCATGCTCCGTGAGCGAAGGCCCTTTTCCCTTCCCTTCCCAATCA	540						
QY	541	GGCGGCTTTTCCCAACCATGAGGACCCCTTCCAGTTCTTCTTCTTTTCTCTC	600						
DB	541	GGCGGCTTTTCCCAACCATGAGGACCCCTTCCAGTTCTTCTTCTTTTCTCTC	600						
QY	601	CCATGCCACCAACCAATGCTTGTCTTAATAACCCCGAGTCCCTGGGGCAGCTTCTTGAC	660						
DB	601	CCATGCCACCAACCAATGCTTGTCTTAATAACCCCGAGTCCCTGGGGCAGCTTCTTGAC	660						
QY	661	AAGGACATTTTCCCTTCAATGATGCCCTTCCCTCCATGCTCATCCCCGGCCCTCCAG	720						
DB	661	AAGGACATTTTCCCTTCAATGATGCCCTTCCCTCCATGCTCATCCCCGGCCCTCCAG	720						

DB	3781	GCTCTTTGGTGAATAATAGAACTCAGGCCAAGTAGCGGAGGAGCTGGGCATCGAGGAGT	3840						
QY	3841	ACGCCATACCAACGACAGACCAAGAGGCGCTGTGGCGCTTCGCAACCAAGACCTTTGGCGG	3900						
DB	3841	ACGCCATACCAACGACAGACCAAGAGGCGCTGTGGCGCTTCGCAACCAAGACCTTTGGCGG	3900						
QY	3901	ACCTTTTGAATCATTTATTGACGCGCTGTACCTGATGAAGATTGGAAATATGTTTCATA	3960						
DB	3901	ACCTTTTGAATCATTTATTGACGCGCTGTACCTGATGAAGATTGGAAATATGTTTCATA	3960						
QY	3961	CTTTCATGAATGCTCTCTTTTCCACGATTCGAAGAAATTCATTTTGAATCAGGATTGGA	4020						
DB	3961	CTTTCATGAATGCTCTCTTTTCCACGATTCGAAGAAATTCATTTTGAATCAGGATTGGA	4020						
QY	4021	ATGACCCCAATCCCAAGCTTCAGCAGTGTGCTTGACCTTAGGACAGAGGAAAGAGC	4080						
DB	4021	ATGACCCCAATCCCAAGCTTCAGCAGTGTGCTTGACCTTAGGACAGAGGAAAGAGC	4080						
QY	4081	CAGACATTCCTCTGTACAAGACTCTGCAGACAGTGGGCCCATCCCATGCCGAACTTACA	4140						
DB	4081	CAGACATTCCTCTGTACAAGACTCTGCAGACAGTGGGCCCATCCCATGCCGAACTTACA	4140						
QY	4141	CTGTGCTGTTTATTTCAAGGAGAAAGATAGCTGTGGAAAGACCAAGTATTTCAGC	4200						
DB	4141	CTGTGCTGTTTATTTCAAGGAGAAAGATAGCTGTGGAAAGACCAAGTATTTCAGC	4200						
QY	4201	AAGCGAAATGGGAGCAGCAATGGATGCGCTTGAAAAATATATTTTCCCGAGATGGCCC	4260						
DB	4201	AAGCGAAATGGGAGCAGCAATGGATGCGCTTGAAAAATATATTTTCCCGAGATGGCCC	4260						
QY	4261	ATCAGAAGCGGTTTCATCGAACGGAAGTACAGACAGAGTTTAAAGAAATGAGTGGGAAA	4320						
DB	4261	ATCAGAAGCGGTTTCATCGAACGGAAGTACAGACAGAGTTTAAAGAAATGAGTGGGAAA	4320						
QY	4321	GAGAGCATCAAGAGAGAGCCGATGAGACTGAGACATCAAGAAATTAAGAGGGGCAT	4380						
DB	4321	GAGAGCATCAAGAGAGAGCCGATGAGACTGAGACATCAAGAAATTAAGAGGGGCAT	4380						
QY	4381	GCAAGTGTGAGTATTTACTTGTCTCAGTAACTGTGACTGTGTCTATTGAGACTAGCCT	4440						
DB	4381	GCAAGTGTGAGTATTTACTTGTCTCAGTAACTGTGACTGTGTCTATTGAGACTAGCCT	4440						
QY	4441	AGTTTTCTCGACGACAAATGAACGAAAGTGTCTCAATGAAATATAAATACAGAGTCAATCG	4500						
DB	4441	AGTTTTCTCGACGACAAATGAACGAAAGTGTCTCAATGAAATATAAATACAGAGTCAATCG	4500						
QY	4501	CTATTGTTGTTTAAATCATCTGTTTTTGTGCTGGATGCTTTTATTAACAAGATTAGATT	4560						
DB	4501	CTATTGTTGTTTAAATCATCTGTTTTTGTGCTGGATGCTTTTATTAACAAGATTAGATT	4560						
QY	4561	TTTCTTCTATTTAACGGAAACTTGACTTTTGGTGAATGTGCATPACTTTCTTTTATTG	4620						
DB	4561	TTTCTTCTATTTAACGGAAACTTGACTTTTGGTGAATGTGCATPACTTTCTTTTATTG	4620						
QY	4621	CTCTTTAAATAATAAATTTCAAGAAGCATATTCATGTGGAATAGATCTGTTTTTCCAT	4680						
DB	4621	CTCTTTAAATAATAAATTTCAAGAAGCATATTCATGTGGAATAGATCTGTTTTTCCAT	4680						
QY	4681	CTGTGCTCCAGATTGTGACCCCTAGACTTTCAATTGACAAAGTAAATAATGACTTTACTAG	4740						
DB	4681	CTGTGCTCCAGATTGTGACCCCTAGACTTTCAATTGACAAAGTAAATAATGACTTTACTAG	4740						
QY	4741	TAAAAAATTT	4764						
DB	4741	TAAAAAATTT	4764						

QY 721 TCATGCGCAGCAGGTTAATTATCAGTACCTTCGGGCTATTCTCACCACAACTTCCCAC 780
DB 721 TCATGCGCAGCAGGTTAATTATCAGTACCTTCGGGCTATTCTCACCACAACTTCCCAC 780
QY 781 CTCCTCAGTTTAAATAGTTTCCAGAAACAACCTTAGTTCTTTCTGCTCCAGTGTCTAATAACA 840
DB 781 CTCCTCAGTTTAAATAGTTTCCAGAAACAACCTTAGTTCTTTCTGCTCCAGTGTCTAATAACA 840
QY 841 GCAGTAGTCTCCTCATTTTTCAGACATCTCCCTCCATACCCACTCCCAAGGCTCCCAAGTGAGA 900
DB 841 GCAGTAGTCTCCTCATTTTTCAGACATCTCCCTCCATACCCACTCCCAAGGCTCCCAAGTGAGA 900
QY 901 GAAGGTCCTCAGAAAGGCTGAAACACTATGATGACCAAGGAGCAGGCGAGTCCCGACAGGA 1020
DB 901 GAAGGTCCTCAGAAAGGCTGAAACACTATGATGACCAAGGAGCAGGCGAGTCCCGACAGGA 1020
QY 961 GCGCAGGTCAGAGGCAATCGGTCCCTCGATCGCGGAGCGAGGCGCAGTCCCGACAGGA 1020
DB 961 GCGCAGGTCAGAGGCAATCGGTCCCTCGATCGCGGAGCGAGGCGCAGTCCCGACAGGA 1020
QY 1021 GAAGACAAGACAGCGGTTACAGATCTGATTATGACCGAGGAGAAACACCATCTCGCCACC 1080
DB 1021 GAAGACAAGACAGCGGTTACAGATCTGATTATGACCGAGGAGAAACACCATCTCGCCACC 1080
QY 1081 GCAGCTACGAAACGAGCAGAGCAGGAGAAACGCGGAGAGACACAGGCAATCGAGACAAACCGAA 1140
DB 1081 GCAGCTACGAAACGAGCAGAGCAGGAGAAACGCGGAGAGACACAGGCAATCGAGACAAACCGAA 1140
QY 1141 GATCACCATCTCTGGAAGGTCCTACAAAGAGGTATTAAGAGTCTGGAAGGAGTTACG 1200
DB 1141 GATCACCATCTCTGGAAGGTCCTACAAAGAGGTATTAAGAGTCTGGAAGGAGTTACG 1200
QY 1201 GTTTATCGGTTGTTCTGAACTGCTGGATGCACACAGAAATTAACCTGGGAGATTAATTA 1260
DB 1201 GTTTATCGGTTGTTCTGAACTGCTGGATGCACACAGAAATTAACCTGGGAGATTAATTA 1260
QY 1261 AAAATACAGATTCTTGGGCCCCACCCCTGGAGATTGTGAATCATCGCTCCCAAGTAGGG 1320
DB 1261 AAAATACAGATTCTTGGGCCCCACCCCTGGAGATTGTGAATCATCGCTCCCAAGTAGGG 1320
QY 1321 AGAAGAAGAGCTGCTGTTGGGAGGAGAAAGACGCTTGGAGTGCACACAGAGTTCTG 1380
DB 1321 AGAAGAAGAGCTGCTGTTGGGAGGAGAAAGACGCTTGGAGTGCACACAGAGTTCTG 1380
QY 1381 GCAAGAACAAGAACTATACCTCAATCAAGGAAAGAGCCCGAGGAGACCATGCTGACA 1440
DB 1381 GCAAGAACAAGAACTATACCTCAATCAAGGAAAGAGCCCGAGGAGACCATGCTGACA 1440
QY 1441 AGAATGAGGAGGAGAAAGAACTTCTTAAGCCTGTGTGATTCGATTCGACTCAATTCAG 1500
DB 1441 AGAATGAGGAGGAGAAAGAACTTCTTAAGCCTGTGTGATTCGATTCGACTCAATTCAG 1500
QY 1501 AAAAATACTACTCCAGTACACCCATGGATCAGTGGGAGATTCTACAGTGTGGAACGA 1560
DB 1501 AAAAATACTACTCCAGTACACCCATGGATCAGTGGGAGATTCTACAGTGTGGAACGA 1560
QY 1561 GTAGGCTTCGTGACTTATGACAAATTTGAGGAGGAGTTGCGGAGCAGGCAAGAAAGG 1620
DB 1561 GTAGGCTTCGTGACTTATGACAAATTTGAGGAGGAGTTGCGGAGCAGGCAAGAAAGG 1620
QY 1621 CCAAAGCTGCTCGGCCCTCCGTTGGAACTCCAAAGACGAAGCTCGATGGAATTTAGAGA 1680
DB 1621 CCAAAGCTGCTCGGCCCTCCGTTGGAACTCCAAAGACGAAGCTCGATGGAATTTAGAGA 1680
QY 1681 GTTCAGTGAATCCAGTGTGAGTCTGATGAGGACAGCACTGTTCTAGCAGCTCAGACT 1740
DB 1681 GTTCAGTGAATCCAGTGTGAGTCTGATGAGGACAGCACTGTTCTAGCAGCTCAGACT 1740
QY 1741 CTGAAGTTTTTGAGCTTATTCAGAAATCAAAACCAAGGCCCCACCTGACCGACTTC 1800
DB 1741 CTGAAGTTTTTGAGCTTATTCAGAAATCAAAACCAAGGCCCCACCTGACCGACTTC 1800

QY 1801 ATGATGAACCTTTTGGTAAACAAGATCCAGGCCAGATGAATGATGACCACTCTGCAAAATGCA 1860
DB 1801 ATGATGAACCTTTTGGTAAACAAGATCCAGGCCAGATGAATGATGACCACTCTGCAAAATGCA 1860
QY 1861 GCGCAAGGCAAGACGACAGGAAATTTAGGACACAGCAATTTATCTGTGAGAAGAGGCCATCA 1920
DB 1861 GCGCAAGGCAAGACGACAGGAAATTTAGGACACAGCAATTTATCTGTGAGAAGAGGCCATCA 1920
QY 1921 AGCCCTGTGCTCTATGACCAACAATGCTGGCAGACTTTTCACTACCGGATCACAAGTCT 1980
DB 1921 AGCCCTGTGCTCTATGACCAACAATGCTGGCAGACTTTTCACTACCGGATCACAAGTCT 1980
QY 1981 CCCCCTACAGAACTTTTAACTGACAGGCCAACTGTTATAGAACTACGATGATCAGAGT 2040
DB 1981 CCCCCTACAGAACTTTTAACTGACAGGCCAACTGTTATAGAACTACGATGATCAGAGT 2040
QY 2041 ATATCTTTGAAGGATTTTCTATGTTTGCACATGCCCCCTGACCAATATTTCCACTGTGTA 2100
DB 2041 ATATCTTTGAAGGATTTTCTATGTTTGCACATGCCCCCTGACCAATATTTCCACTGTGTA 2100
QY 2101 AAGTAATTAGATTCAACATAGACTACAGATTCAATTCATTGAAGAGATGATCCGGAGA 2160
DB 2101 AAGTAATTAGATTCAACATAGACTACAGATTCAATTCATTGAAGAGATGATCCGGAGA 2160
QY 2161 ATTTTGTGTGAAGGGCTTGAACCTTTTCACTGTTCTATTTCAGAGATATTTTGGAAT 2220
DB 2161 ATTTTGTGTGAAGGGCTTGAACCTTTTCACTGTTCTATTTCAGAGATATTTTGGAAT 2220
QY 2221 TATATGACTGGAACTTTAAAGGCTTTTGTGTTGAAGACAGCCCTCTGCTGCCCAAGAT 2280
DB 2221 TATATGACTGGAACTTTAAAGGCTTTTGTGTTGAAGACAGCCCTCTGCTGCCCAAGAT 2280
QY 2281 TTCACTTCATGCGCACTTTTGAAGTTTCTTCCAGATGGAAGAAAGTGTGTCCA 2340
DB 2281 TTCACTTCATGCGCACTTTTGAAGTTTCTTCCAGATGGAAGAAAGTGTGTCCA 2340
QY 2341 TGCAACAGATTCTCCTGTACTTGTGTTAAGGTGCAAAAGCCCTGCTGCTGAGGAGGAGA 2400
DB 2341 TGCAACAGATTCTCCTGTACTTGTGTTAAGGTGCAAAAGCCCTGCTGCTGAGGAGGAGA 2400
QY 2401 TTGCCAATATCTTTCAGTGGGAGGAGCTGGAGTGGCAGAAATATGCAAGAAGATGCAAG 2460
DB 2401 TTGCCAATATCTTTCAGTGGGAGGAGCTGGAGTGGCAGAAATATGCAAGAAGATGCAAG 2460
QY 2461 GCATGATTGTTTACCAACCCCTGGAGCAACCAAGCTCTGTCGTATCGATCAACTGGATC 2520
DB 2461 GCATGATTGTTTACCAACCCCTGGAGCAACCAAGCTCTGTCGTATCGATCAACTGGATC 2520
QY 2521 GTGAACAGTTTCAACCCCGATGATTACTTTTCCGATTTATCGTCCACTTTGGGATACGCC 2580
DB 2521 GTGAACAGTTTCAACCCCGATGATTACTTTTCCGATTTATCGTCCACTTTGGGATACGCC 2580
QY 2581 CTGCACAGTTGAGTTATGCAAGGAGACCAAGTACCAAACTGTTGGAAGAGTTATGTGA 2640
DB 2581 CTGCACAGTTGAGTTATGCAAGGAGACCAAGTACCAAACTGTTGGAAGAGTTATGTGA 2640
QY 2641 AACTTCCGCACTCTTACGCAAAATAGTCCCAAGTCAACAACTGCAAAAACAGAGCTGG 2700
DB 2641 AACTTCCGCACTCTTACGCAAAATAGTCCCAAGTCAACAACTGCAAAAACAGAGCTGG 2700
QY 2701 CACAGAGGAGGAGGAGCCCTCCAAAAATAACGCGAAGAAATACAAATGAGACGAGAGTAA 2760
DB 2701 CACAGAGGAGGAGGAGCCCTCCAAAAATAACGCGAAGAAATACAAATGAGACGAGAGTAA 2760
QY 2761 CGGTGAGGAGTTAAGTACCAAGGATTTGGAATACTGGGATCCGTTCTGATGCTGTGTCAGC 2820
DB 2761 CGGTGAGGAGTTAAGTACCAAGGATTTGGAATACTGGGATCCGTTCTGATGCTGTGTCAGC 2820
QY 2821 ATGCAATGATGCTACCTGTTCTGACCCCATCATATCCGCTACCAACCAATGCTTAATGATT 2880
DB 2821 ATGCAATGATGCTACCTGTTCTGACCCCATCATATCCGCTACCAACCAATGCTTAATGATT 2880
QY 2881 TGGACAAGTTTGATAGGATATATCTTTTCCAAGATCGTTGCTGTGTCAGCTGGCCATGACTC 2940

QY	3121	CCTCGAGGATTAACCAATGAACGGTGGAAATTCCTGGGTGATGCTGTGTTGAATTC	3180
Db	3121	CCTCGAGGATTAACCAATGAACGGTGGAAATTCCTGGGTGATGCTGTGTTGAATTC	3180
QY	3181	TGACGAGCGTCCATTGTGTAATAATTTGTTCTAGTCTGGAAGAAGGAGGATTAGCAACCT	3240
Db	3181	TGACGAGCGTCCATTGTGTAATAATTTGTTCTAGTCTGGAAGAAGGAGGATTAGCAACCT	3240
QY	3181	TGACGAGCGTCCATTGTGTAATAATTTGTTCTAGTCTGGAAGAAGGAGGATTAGCAACCT	3240
Db	3181	TGACGAGCGTCCATTGTGTAATAATTTGTTCTAGTCTGGAAGAAGGAGGATTAGCAACCT	3240
QY	3241	ATCGGACCTGCATTGTTTCAGAAATCAGCAACCTTGCCATGCTAGCAAGAACTTGAACCTGG	3300
Db	3241	ATCGGACCTGCATTGTTTCAGAAATCAGCAACCTTGCCATGCTAGCAAGAACTTGAACCTGG	3300
QY	3241	ATCGGACCTGCATTGTTTCAGAAATCAGCAACCTTGCCATGCTAGCAAGAACTTGAACCTGG	3300
Db	3241	ATCGGACCTGCATTGTTTCAGAAATCAGCAACCTTGCCATGCTAGCAAGAACTTGAACCTGG	3300
QY	3301	ATCCATTTATGCTGATGCTCAAGGCGCTGACCTTTGTAGAGAATCGGACCTTCGACATG	3360
Db	3301	ATCCATTTATGCTGATGCTCAAGGCGCTGACCTTTGTAGAGAATCGGACCTTCGACATG	3360
QY	3301	ATCCATTTATGCTGATGCTCAAGGCGCTGACCTTTGTAGAGAATCGGACCTTCGACATG	3360
Db	3301	ATCCATTTATGCTGATGCTCAAGGCGCTGACCTTTGTAGAGAATCGGACCTTCGACATG	3360
QY	3361	CAATGGCCCAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTTGAGAGGAAGCCTGGAGG	3420
Db	3361	CAATGGCCCAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTTGAGAGGAAGCCTGGAGG	3420
QY	3361	CAATGGCCCAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTTGAGAGGAAGCCTGGAGG	3420
Db	3361	CAATGGCCCAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTTGAGAGGAAGCCTGGAGG	3420
QY	3421	AAGCCAAAGCAATTTTGGACGCTTCTCTCTTTAAATGATCCGACCTGCGGAGTCTGGC	3480
Db	3421	AAGCCAAAGCAATTTTGGACGCTTCTCTCTTTAAATGATCCGACCTGCGGAGTCTGGC	3480
QY	3421	AAGCCAAAGCAATTTTGGACGCTTCTCTCTTTAAATGATCCGACCTGCGGAGTCTGGC	3480
Db	3421	AAGCCAAAGCAATTTTGGACGCTTCTCTCTTTAAATGATCCGACCTGCGGAGTCTGGC	3480
QY	3481	TCAATTTATCTCTCCACCACTCCAACTAAGAGCGCAATATCTGATCGCAACTTATTG	3540
Db	3481	TCAATTTATCTCTCCACCACTCCAACTAAGAGCGCAATATCTGATCGCAACTTATTG	3540
QY	3481	TCAATTTATCTCTCCACCACTCCAACTAAGAGCGCAATATCTGATCGCAACTTATTG	3540
Db	3481	TCAATTTATCTCTCCACCACTCCAACTAAGAGCGCAATATCTGATCGCAACTTATTG	3540
QY	3541	AAAATTTCTCCAGTTCTACAATACTTACGTTTGAAGAGCAATTTGGAGTAAATTTT	3600
Db	3541	AAAATTTCTCCAGTTCTACAATACTTACGTTTGAAGAGCAATTTGGAGTAAATTTT	3600
QY	3541	AAAATTTCTCCAGTTCTACAATACTTACGTTTGAAGAGCAATTTGGAGTAAATTTT	3600
Db	3541	AAAATTTCTCCAGTTCTACAATACTTACGTTTGAAGAGCAATTTGGAGTAAATTTT	3600
QY	3601	CTCATGTTCTGCACTTCTGCGAAGGCAATTCATTTGAGAACTGTGGGATTTAACCATCTGA	3660
Db	3601	CTCATGTTCTGCACTTCTGCGAAGGCAATTCATTTGAGAACTGTGGGATTTAACCATCTGA	3660
QY	3601	CTCATGTTCTGCACTTCTGCGAAGGCAATTCATTTGAGAACTGTGGGATTTAACCATCTGA	3660
Db	3601	CTCATGTTCTGCACTTCTGCGAAGGCAATTCATTTGAGAACTGTGGGATTTAACCATCTGA	3660
QY	3661	CCCTAGGCGACCAATCAGAGAATGGAATTCCTAGGTGACTCCATTAATGCAACTGGTAGCCA	3720
Db	3661	CCCTAGGCGACCAATCAGAGAATGGAATTCCTAGGTGACTCCATTAATGCAACTGGTAGCCA	3720
QY	3661	CCCTAGGCGACCAATCAGAGAATGGAATTCCTAGGTGACTCCATTAATGCAACTGGTAGCCA	3720
Db	3661	CCCTAGGCGACCAATCAGAGAATGGAATTCCTAGGTGACTCCATTAATGCAACTGGTAGCCA	3720
QY	3721	CAGAGTACTTATTTCAATTTCCAGATCATGAAAGGACACTTAACTTTGTTGGCAA	3780
Db	3721	CAGAGTACTTATTTCAATTTCCAGATCATGAAAGGACACTTAACTTTGTTGGCAA	3780
QY	3721	CAGAGTACTTATTTCAATTTCCAGATCATGAAAGGACACTTAACTTTGTTGGCAA	3780
Db	3721	CAGAGTACTTATTTCAATTTCCAGATCATGAAAGGACACTTAACTTTGTTGGCAA	3780
QY	3781	GCTCTTTGGTGAATATAGAACTCAGGCCAAGGTAGCGAGAGCTGGCATGCAAGGAT	3840
Db	3781	GCTCTTTGGTGAATATAGAACTCAGGCCAAGGTAGCGAGAGCTGGCATGCAAGGAT	3840
QY	3781	GCTCTTTGGTGAATATAGAACTCAGGCCAAGGTAGCGAGAGCTGGCATGCAAGGAT	3840
Db	3781	GCTCTTTGGTGAATATAGAACTCAGGCCAAGGTAGCGAGAGCTGGCATGCAAGGAT	3840
QY	3841	ACGCCATAACCAAGCAAGCAAGAGGCGCTGTGGGCTTCGCACCAAGACCTTGGCGG	3900
Db	3841	ACGCCATAACCAAGCAAGCAAGAGGCGCTGTGGGCTTCGCACCAAGACCTTGGCGG	3900
QY	3841	ACGCCATAACCAAGCAAGCAAGAGGCGCTGTGGGCTTCGCACCAAGACCTTGGCGG	3900
Db	3841	ACGCCATAACCAAGCAAGCAAGAGGCGCTGTGGGCTTCGCACCAAGACCTTGGCGG	3900
QY	3901	ACCTTTTGGATCATTTATTTGACGCGCTGTACCTGATAGGAATTTTGGAAATATGTTCA	3960
Db	3901	ACCTTTTGGATCATTTATTTGACGCGCTGTACCTGATAGGAATTTTGGAAATATGTTCA	3960
QY	3901	ACCTTTTGGATCATTTATTTGACGCGCTGTACCTGATAGGAATTTTGGAAATATGTTCA	3960
Db	3901	ACCTTTTGGATCATTTATTTGACGCGCTGTACCTGATAGGAATTTTGGAAATATGTTCA	3960
QY	3961	CTTTTCATGAATGTCTGCTTCTTCCAGATTTGAAGAATTTCAATTTGAATCAGAGTTGGA	4020
Db	3961	CTTTTCATGAATGTCTGCTTCTTCCAGATTTGAAGAATTTCAATTTGAATCAGAGTTGGA	4020
QY	3961	CTTTTCATGAATGTCTGCTTCTTCCAGATTTGAAGAATTTCAATTTGAATCAGAGTTGGA	4020
Db	3961	CTTTTCATGAATGTCTGCTTCTTCCAGATTTGAAGAATTTCAATTTGAATCAGAGTTGGA	4020
QY	4021	ATGACCCCAAAATCCAGCTTCAGCAGTGTGTTGACACTTAGCAGAGAGGAAAAGAGC	4080
Db	4021	ATGACCCCAAAATCCAGCTTCAGCAGTGTGTTGACACTTAGCAGAGAGGAAAAGAGC	4080
QY	4021	ATGACCCCAAAATCCAGCTTCAGCAGTGTGTTGACACTTAGCAGAGAGGAAAAGAGC	4080
Db	4021	ATGACCCCAAAATCCAGCTTCAGCAGTGTGTTGACACTTAGCAGAGAGGAAAAGAGC	4080
QY	4081	CAGACATTTCTCTGTACAAGCTCTGACAGAGTGGGCCATCCCATGCGGAACTTACA	4140
Db	4081	CAGACATTTCTCTGTACAAGCTCTGACAGAGTGGGCCATCCCATGCGGAACTTACA	4140
QY	4081	CAGACATTTCTCTGTACAAGCTCTGACAGAGTGGGCCATCCCATGCGGAACTTACA	4140
Db	4081	CAGACATTTCTCTGTACAAGCTCTGACAGAGTGGGCCATCCCATGCGGAACTTACA	4140
QY	4141	CTGTGGCTGTGTTTATTTCAAGGGGAGAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTCAGC	4200
Db	4141	CTGTGGCTGTGTTTATTTCAAGGGGAGAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTCAGC	4200
QY	4141	CTGTGGCTGTGTTTATTTCAAGGGGAGAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTCAGC	4200
Db	4141	CTGTGGCTGTGTTTATTTCAAGGGGAGAAAGAAATAGGCTGTGGGAAAGGACCAAGTATTCAGC	4200
QY	4201	AAGCGGAAATGGGGAGCAGCAATGGATGCGCTTGAAATAATATATTTTCCCAGATGGCCC	4260

QY	1141	GATCACCATCTCTGGAAAGGTCCTCA	CAAAAAAGAGTATTAAGAGATCTGGAAGAGTTACG	1200
DB	1141	GATCACCATCTCTGGAAAGGTCCTCA	CAAAAAAGAGTATTAAGAGATCTGGAAGAGTTACG	1200
QY	1201	GTATTATCGGTTGTTCTGACCTGCTG	GAATGACACACAGAAATTTACCTGGGGAGATTATTA	1260
DB	1201	GTATTATCGGTTGTTCTGACCTGCTG	GAATGACACACAGAAATTTACCTGGGGAGATTATTA	1260
QY	1261	AAAATACAGATTTCTGGGCCCCCACC	CTCGAGATTTGTGAATCATCGTCCCCAAAGTAGGG	1320
DB	1261	AAAATACAGATTTCTGGGCCCCCACC	CTCGAGATTTGTGAATCATCGTCCCCAAAGTAGGG	1320
QY	1321	AGAAGAAGAGAGCTCGTTGGGAGGA	AGAAAAAGACCGTTGGAGTGAACACACAGAGTTCTG	1380
DB	1321	AGAAGAAGAGAGCTCGTTGGGAGGA	AGAAAAAGACCGTTGGAGTGAACACACAGAGTTCTG	1380
QY	1381	GCAAGACAGAACTATACCTCAATCA	AGGAAAGAGCCGAGGAGACCATCGCTTGACA	1440
DB	1381	GCAAGACAGAACTATACCTCAATCA	AGGAAAGAGCCGAGGAGACCATCGCTTGACA	1440
QY	1441	AGAATGAGGAGGAAGAAGAACTTCT	TAAAGCCTGTGTGGATTCGATGCACCTCATTTAG	1500
DB	1441	AGAATGAGGAGGAAGAAGAACTTCT	TAAAGCCTGTGTGGATTCGATGCACCTCATTTAG	1500
QY	1501	AAAACTACTACTCCAGTGAACCCAT	GGATCAGGTGGGAGATTCTACAGTGGTTGGAAACGA	1560
DB	1501	AAAACTACTACTCCAGTGAACCCAT	GGATCAGGTGGGAGATTCTACAGTGGTTGGAAACGA	1560
QY	1561	GTAGGCTTCTGTGACTTATATGACA	AAATTTGAGGAGGAGTTGGGGAGCAGGCAAGAAAGG	1620
DB	1561	GTAGGCTTCTGTGACTTATATGACA	AAATTTGAGGAGGAGTTGGGGAGCAGGCAAGAAAGG	1620
QY	1621	CAAAAGCTGCTCGGCTCCGTGGAA	CTCCAAAGACGAAGCTCGATGAAGATTATGAGA	1680
DB	1621	CAAAAGCTGCTCGGCTCCGTGGAA	CTCCAAAGACGAAGCTCGATGAAGATTATGAGA	1680
QY	1681	GTTCCAGTGAATCCGAGTGTGAGT	CTGATGAGGACGACACTGTTCTTAGCAGCTCAGACT	1740
DB	1681	GTTCCAGTGAATCCGAGTGTGAGT	CTGATGAGGACGACACTGTTCTTAGCAGCTCAGACT	1740
QY	1741	CTGAAGTTTTTGAGTTTATTCGAA	NTCAAAAGGAGGCCCCACCTCGACGACTTC	1800
DB	1741	CTGAAGTTTTTGAGTTTATTCGAA	NTCAAAAGGAGGCCCCACCTCGACGACTTC	1800
QY	1801	ATGATGAACCTTTGTTCAACGAT	CCAGGCCAGATGAATGATGACCACTCTGCAAAATGCA	1860
DB	1801	ATGATGAACCTTTGTTCAACGAT	CCAGGCCAGATGAATGATGACCACTCTGCAAAATGCA	1860
QY	1861	GCGCAAGGCAAGACGACAGGAAT	TAGGCAAGCATTTATCTCTGGAGAGAGGCCATCA	1920
DB	1861	GCGCAAGGCAAGACGACAGGAAT	TAGGCAAGCATTTATCTCTGGAGAGAGGCCATCA	1920
QY	1921	AGCCCTGTCTCTATGACCAACAT	GCTGGCAGACTTTTCCATACCGGATCAGCTCT	1980
DB	1921	AGCCCTGTCTCTATGACCAACAT	GCTGGCAGACTTTTCCATACCGGATCAGCTCT	1980
QY	1981	CCCGCCTACCAACTTTTAACTG	CACAGGCCAACTGTTATAGATACGATGATCAGAGT	2040
DB	1981	CCCGCCTACCAACTTTTAACTG	CACAGGCCAACTGTTATAGATACGATGATCAGAGT	2040
QY	2041	ATATCTTTGAAGGATTTTCTATG	TTTGCAATGCCCCCTCGAACCAATATTCCA	2100
DB	2041	ATATCTTTGAAGGATTTTCTATG	TTTGCAATGCCCCCTCGAACCAATATTCCA	2100
QY	2101	AAGTAATTAGATTCAACATAGAC	TACACGATTTCAATTTGAAGAGATGATCGCGAGA	2160
DB	2101	AAGTAATTAGATTCAACATAGAC	TACACGATTTCAATTTGAAGAGATGATCGCGAGA	2160
QY	2161	ATTTTGTGTCAAAAGGGCTTGA	ATCTTTTCACTGTTCCCTATTTCAGAGATATTTTGAAT	2220
DB	2161	ATTTTGTGTCAAAAGGGCTTGA	ATCTTTTCACTGTTCCCTATTTCAGAGATATTTTGAAT	2220

QY	2221	TATATGACTGGAACTTTAAAGGT	CTTTTGTGTTGAAGACAGACCCCTCCCTGCTGC	2280
DB	2221	TATATGACTGGAACTTTAAAGGT	CTTTTGTGTTGAAGACAGACCCCTCCCTGCTGC	2280
QY	2281	TTCAATTTCAATCCACGTTTTTGA	AGATTTCTTCCAGATGGAGAAAGGAAGTCTGTCCA	2340
DB	2281	TTCAATTTCAATCCACGTTTTTGA	AGATTTCTTCCAGATGGAGAAAGGAAGTCTGTCCA	2340
QY	2341	TGCACACAGATTTCTCTGTACT	TTTAAAGGTGAGCAAAAGCCCTGGTGCCTGAGGAGGAGA	2400
DB	2341	TGCACACAGATTTCTCTGTACT	TTTAAAGGTGAGCAAAAGCCCTGGTGCCTGAGGAGGAGA	2400
QY	2401	TTGCCAATATGCTTCAGTGGGAG	GAGCTGGAGTATGAGAAATATGAGAAAGATGCAAAAG	2460
DB	2401	TTGCCAATATGCTTCAGTGGGAG	GAGCTGGAGTATGAGAAATATGAGAAAGATGCAAAAG	2460
QY	2461	GCATGATTTGTACCAACCCCTG	GGAACGAAACCAAGCTCTGTCCGTATCGATCAACTG	2520
DB	2461	GCATGATTTGTACCAACCCCTG	GGAACGAAACCAAGCTCTGTCCGTATCGATCAACTG	2520
QY	2521	GTGAACAGTTTCAACCCCGAT	GTGATTACTTTTCCGATTATCGTCCACTTTTGGGATACGCC	2580
DB	2521	GTGAACAGTTTCAACCCCGAT	GTGATTACTTTTCCGATTATCGTCCACTTTTGGGATACGCC	2580
QY	2581	CTGCACAGTTGAGTTATGACAG	GAGACCCACAGTACCAAAAATCTGTGGAAAGATTATGTGA	2640
DB	2581	CTGCACAGTTGAGTTATGACAG	GAGACCCACAGTACCAAAAATCTGTGGAAAGATTATGTGA	2640
QY	2641	AACTTCGCCCACTCTCTAGCA	AAATAGTCCCAAAAGTCAAAACAACTGACAAACAGAACTGG	2700
DB	2641	AACTTCGCCCACTCTCTAGCA	AAATAGTCCCAAAAGTCAAAACAACTGACAAACAGAACTGG	2700
QY	2701	CACAGAGGAGGAGCCCTCCAA	AAATAGCGCAGAGAAATACAATGAGACGAGAAAGTAA	2760
DB	2701	CACAGAGGAGGAGCCCTCCAA	AAATAGCGCAGAGAAATACAATGAGACGAGAAAGTAA	2760
QY	2761	CGGTGAGCTTAAGTACCAAG	ATTCTGGAAAACTGGCATCCCTTCTGTGATGTCTGCAGC	2820
DB	2761	CGGTGAGCTTAAGTACCAAG	ATTCTGGAAAACTGGCATCCCTTCTGTGATGTCTGCAGC	2820
QY	2821	ATGCAATGATGTCTGTTCTG	ACCCATCATATCCGCTACCAACCAATGCTTAATGCAAT	2880
DB	2821	ATGCAATGATGTCTGTTCTG	ACCCATCATATCCGCTACCAACCAATGCTTAATGCAAT	2880
QY	2881	TGACCAAGTTGATAGATATAC	TTTCCAGATCGTTGTTGTCAGCTGCGCATGACTC	2940
DB	2881	TGACCAAGTTGATAGATATAC	TTTCCAGATCGTTGTTGTCAGCTGCGCATGACTC	2940
QY	2941	ATCCAACTCATATTTAAAT	TTTGGAAATGAAATCTGATCATGCGAGGAATTCATTA	3000
DB	2941	ATCCAACTCATATTTAAAT	TTTGGAAATGAAATCTGATCATGCGAGGAATTCATTA	3000
QY	3001	ACTGTGGAATTCGGCAGCCCA	ATAACGAGACAGAAAGTTTCATCATGCAATGCGGA	3060
DB	3001	ACTGTGGAATTCGGCAGCCCA	ATAACGAGACAGAAAGTTTCATCATGCAATGCGGA	3060
QY	3061	AGAAAGGATTAACACCTTGT	ATAATCATGTCAACGCTTGGCCAGAGTACCCAACTC	3120
DB	3061	AGAAAGGATTAACACCTTGT	ATAATCATGTCAACGCTTGGCCAGAGTACCCAACTC	3120
QY	3121	CCTCGAGATTAACCAATGA	ACGGTTGGAATTTCTGGGTGATGCTGTTGTAATTC	3180
DB	3121	CCTCGAGATTAACCAATGA	ACGGTTGGAATTTCTGGGTGATGCTGTTGTAATTC	3180
QY	3181	TGACACAGCTCCATTTGTACT	ATTTTGTCTAGTCTGGAAGAGAGGAGATTAGCAACCT	3240
DB	3181	TGACACAGCTCCATTTGTACT	ATTTTGTCTAGTCTGGAAGAGAGGAGATTAGCAACCT	3240
QY	3241	ATCGGACTGCAATTTGTTCA	GAATCAGCACTTGCCTAGCAGAAAGAACTTGAACCTGG	3300
DB	3241	ATCGGACTGCAATTTGTTCA	GAATCAGCACTTGCCTAGCAGAAAGAACTTGAACCTGG	3300
QY	3301	ATCCATTTATGCTGATGCT	CAACGGGCTGACCTTTTGTAGAGATCGGACCTTCGACATG	3360

QY 4681 CTGTGTCACAGATGTGACCCCTAGACTTCAATTTGACAAAGTAAATAATGACTTTACTAG 4740
Db |||||||
QY 4681 CTGTGTCACAGATGTGACCCCTAGACTTCAATTTGACAAAGTAAATAATGACTTTACTAG 4740
Db |||||||
QY 4741 TAAAAAATAAAAAAAAAAAAAA 4764
Db |||||||
QY 4741 TAAAAAATAAAAAAAAAAAAAA 4764
Db |||||||

RESULT 7
US-10-756-149-319
; Sequence 319, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 319
; LENGTH: 4764
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-319

Query Match 99.9%; Score 4760.8; DB 9; Length 4764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4762; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGTCTTGTTGTTACCTGCGGTAGTACCTGGCTTTGCTCTGACGCGCATCTCGCGGCCGAG 60
Db |||||||
QY 1 CTGTCTTGTTGTTACCTGCGGTAGTACCTGGCTTTGCTCTGACGCGCATCTCGCGGCCGAG 60
Db |||||||
QY 61 AGCCTTTTATAGTTGCTTTTCCCGGGATGTGAAGATATACAGAAATGACTGTGAATCAA 120
Db |||||||
QY 61 AGCCTTTTATAGTTGCTTTTCCCGGGATGTGAAGATATACAGAAATGACTGTGAATCAA 120
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QY 121 CCCATATCATCAAGGAGCTGATAATCTAGTGGAAAGATTAGACGTGTGCATCTTCACTA 180
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QY 181 TGATATGAGGAGTCTCTGAGCTTATATTCTCTGTGGAAGATGTGACATATCCAGGCGGA 240
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QY 301 CCCGAGGACGAGGAGGACATGAGCCAGACCTCTGAGCCATCTTTAGGCCCCCAAAATC 360
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QY 361 TGAGGCTGCTTCACTCAGGAGCTCTGTGCAATATCAATATGAACTTCAAGTGGCC 420
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QY 361 TGAGGCTGCTTCACTCAGGAGCTCTGTGCAATATCAATATGAACTTCAAGTGGCC 420
Db |||||||
QY 421 CTTCACCACTTCTCAAACTCTCAGGCCCAATTTTCTCCCTCCAGCACGACTTTG 480
Db |||||||
QY 421 CTTCACCACTTCTCAAACTCTCAGGCCCAATTTTCTCCCTCCAGCACGACTTTG 480
Db |||||||
QY 481 TACCTCTCCGCCACCCATGCTCCGTCAGGCAAGGCGCTTCTCCGCCCTGCCAATCA 540
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QY 601 CCATGCCACCACCAATGCTTGTCTCTAATAACCCCTCAGTCCCTGGGGCACCTCTCTGAC 660
Db |||||||
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Db |||||||
QY 661 AAGGCACTTTTCCCTTTCATGATGCCCCCTCTCATGCTCATCCCGGCCCTCCAG 720
Db |||||||
QY 721 TCATGCCGAGCAGGTTAATTTATCAGTACCTTCCGGGCTATTTCTCACCACAATTTCCAC 780
Db |||||||
QY 721 TCATGCCGAGCAGGTTAATTTATCAGTACCTTCCGGGCTATTTCTCACCACAATTTCCAC 780
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QY 781 CTCCTCAGTTTAAATAGTTTTCAGAAACACCTTAGTTCTTTCTGCTGCCAGTGTAAATA 840
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QY 781 CTCCTCAGTTTAAATAGTTTTCAGAAACACCTTAGTTCTTTCTGCTGCCAGTGTAAATA 840
Db |||||||
QY 841 GCAGTAGTCTCTCATTTTCAGACATCTCCCTCCATACCCACTCCCAAAGGCTCCAGTGAGA 900
Db |||||||
QY 841 GCAGTAGTCTCTCATTTTCAGACATCTCCCTCCATACCCACTCCCAAAGGCTCCAGTGAGA 900
Db |||||||
QY 901 GAAGTCTCCCAAGAAAGGCTGAAACACATATGATGACACAGGACCGAGACACAGTCATG 960
Db |||||||
QY 901 GAAGTCTCCCAAGAAAGGCTGAAACACATATGATGACACAGGACCGAGACACAGTCATG 960
Db |||||||
QY 961 GCGGAGTGCAGAGGATCGGTCCCTGGATCGCGGGAGCGAGCCCGCAGTCCCGACAGGA 1020
Db |||||||
QY 961 GCGGAGTGCAGAGGATCGGTCCCTGGATCGCGGGAGCGAGCCCGCAGTCCCGACAGGA 1020
Db |||||||
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QY 1081 GCAGTACGAAACGAGCAGACGAGAACCGGAGAGACACAGGATCTGAGAACACCGAA 1140
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QY 1081 GCAGTACGAAACGAGCAGACGAGAACCGGAGAGACACAGGATCTGAGAACACCGAA 1140
Db |||||||
QY 1141 GATCCATCTCTGGAAGGTCCTACAAAAACAGATTAAGAGATCTGGAAGAGGTTACG 1200
Db |||||||
QY 1141 GATCCATCTCTGGAAGGTCCTACAAAAACAGATTAAGAGATCTGGAAGAGGTTACG 1200
Db |||||||
QY 1201 GTTTATCGGTTGTTCTCTGAACTCTGATGACACACAGAAATTTACCTGGGAGATTATTA 1260
Db |||||||
QY 1201 GTTTATCGGTTGTTCTCTGAACTCTGATGACACACAGAAATTTACCTGGGAGATTATTA 1260
Db |||||||
QY 1261 AAAATACAGATTTCTGGGCCCCACCTTGGAGATTTGAAATCATCGCTCCCAAGTAGGG 1320
Db |||||||
QY 1261 AAAATACAGATTTCTGGGCCCCACCTTGGAGATTTGAAATCATCGCTCCCAAGTAGGG 1320
Db |||||||
QY 1321 AGAAGAGAGAGCTCGTTGGGAGGAGAAAAAGACCGTTGGAGTGACAAACAGAGTTCTG 1380
Db |||||||
QY 1321 AGAAGAGAGAGCTCGTTGGGAGGAGAAAAAGACCGTTGGAGTGACAAACAGAGTTCTG 1380
Db |||||||
QY 1381 GCAAGACAAAGAACTATACCTCAATCAAGGAAAAAGACCGCGGAGAGACCATGCTGACA 1440
Db |||||||
QY 1381 GCAAGACAAAGAACTATACCTCAATCAAGGAAAAAGACCGCGGAGAGACCATGCTGACA 1440
Db |||||||
QY 1441 AGAATGAGGAGGAGAAAGAACTTCTTAAGCCTGTGTGATTCGATGCACTCATTTAG 1500
Db |||||||
QY 1441 AGAATGAGGAGGAGAAAGAACTTCTTAAGCCTGTGTGATTCGATGCACTCATTTAG 1500
Db |||||||
QY 1501 AAAACTACTACTCCAGTGACCCCATGATCAGGTGGGAGATTCTTACAGTGGTTGGAACGA 1560
Db |||||||
QY 1501 AAAACTACTACTCCAGTGACCCCATGATCAGGTGGGAGATTCTTACAGTGGTTGGAACGA 1560
Db |||||||
QY 1561 GTAGGCTTCTGATCTTATATGACAAATTTGAGGAGGAGTTGGGAGCAGGCAAGAAAGG 1620
Db |||||||
QY 1561 GTAGGCTTCTGATCTTATATGACAAATTTGAGGAGGAGTTGGGAGCAGGCAAGAAAGG 1620
Db |||||||
QY 1621 CCAAAGTGTCTCGGCTCCGTTGGGAACTCTCAAGAGAGAGCTCGATTAAGATTAGAGA 1680
Db |||||||
QY 1621 CCAAAGTGTCTCGGCTCCGTTGGGAACTCTCAAGAGAGAGCTCGATTAAGATTAGAGA 1680
Db |||||||

1681 GTTCCAGTGAATCCGAGTGTGAGTCTGATGAGGACGACACCTGTTCTAGCAGCTCAGACT 1740
1681 GTTCCAGTGAATCCGAGTGTGAGTCTGATGAGGACGACACCTGTTCTAGCAGCTCAGACT 1740
1741 CTGAAGTTTTTGACGTTATTTGACAGAAATCAAAACGAAAAAGGCCACCTGACCGACTTC 1800
1741 CTGAAGTTTTTGACGTTATTTGACAGAAATCAAAACGAAAAAGGCCACCTGACCGACTTC 1800
1801 ATGATGAATCTTGTGTACAAACGATCCAGGCCAGATGAATGATGAGCACTCTGCAAAATGCA 1860
1801 ATGATGAATCTTGTGTACAAACGATCCAGGCCAGATGAATGATGAGCACTCTGCAAAATGCA 1860
1861 GCGCAAGGCAAGACGACAGCAAGAAATAGGACACATTTATCTTGGAGAGAGAGGCCATCA 1920
1861 GCGCAAGGCAAGACGACAGCAAGAAATAGGACACATTTATCTTGGAGAGAGAGGCCATCA 1920
1921 AGCCCTGTCTGCTATGACCAACAACTGTCGACAGATTTTCCACTACCGGATCACAGTCT 1980
1921 AGCCCTGTCTGCTATGACCAACAACTGTCGACAGATTTTCCACTACCGGATCACAGTCT 1980
1981 CCCGCCCTACGAATTTTAACTGACAGGCCAACTGTTATAGAAATACGATGATCACAGT 2040
1981 CCCGCCCTACGAATTTTAACTGACAGGCCAACTGTTATAGAAATACGATGATCACAGT 2040
2041 ATATCTTTGAAGGATTTTCTATGTTGACATGCCCCCTGACCAATATTTCCACTGTGTA 2100
2041 ATATCTTTGAAGGATTTTCTATGTTGACATGCCCCCTGACCAATATTTCCACTGTGTA 2100
2101 AAGTAATTAGAATCAACATAGACTACACAGATTCATTTCAATGAGAGATGATGCCGAGA 2160
2101 AAGTAATTAGAATCAACATAGACTACACAGATTCATTTCAATGAGAGATGATGCCGAGA 2160
2161 ATTTTGTGTGAAGGCTTGAATCTTTTCACTGTTTCACTGTTTCTTATTCAGAGATATTTTGAAT 2220
2161 ATTTTGTGTGAAGGCTTGAATCTTTTCACTGTTTCACTGTTTCTTATTCAGAGATATTTTGAAT 2220
2221 TATATGACTGGAATCTTAAAGTCTTTGTTGAGACAGCCCTCCTGTCGCCAAGAT 2280
2221 TATATGACTGGAATCTTAAAGTCTTTGTTGAGACAGCCCTCCTGTCGCCAAGAT 2280
2281 TTCAATTTATGTCACAGTCTTAAAGTCTTTGTTGAGACAGCCCTCCTGTCGCCAAGAT 2340
2281 TTCAATTTATGTCACAGTCTTAAAGTCTTTGTTGAGACAGCCCTCCTGTCGCCAAGAT 2340
2341 TGCAACAGATTTCTGTAATTTGTTAAGGTGACAGAAAGCCCTGTCGCCAAGAT 2400
2341 TGCAACAGATTTCTGTAATTTGTTAAGGTGACAGAAAGCCCTGTCGCCAAGAT 2400
2401 TTGCCAATATGCTTCAAGTGGAGGAGCTGGAGTGGCAGAAATATGCAAGAAATGCAAG 2460
2401 TTGCCAATATGCTTCAAGTGGAGGAGCTGGAGTGGCAGAAATATGCAAGAAATGCAAG 2460
2461 GCATGATTTTACCAACCTGGGACGAAACCAAGTCTGTCGATCGATCAACTGGATC 2520
2461 GCATGATTTTACCAACCTGGGACGAAACCAAGTCTGTCGATCGATCAACTGGATC 2520
2521 GTGAACAGTTCAACCCCGATGTGATTTTCCGATTTATCGTCCACTTTGGGATACGCC 2580
2521 GTGAACAGTTCAACCCCGATGTGATTTTCCGATTTATCGTCCACTTTGGGATACGCC 2580
2581 CTGACAGTTGAGTTATGACAGGAGACCCACAGTACCAAACTGTTGGAAGAGTTATGTA 2640
2581 CTGACAGTTGAGTTATGACAGGAGACCCACAGTACCAAACTGTTGGAAGAGTTATGTA 2640
2641 AACTTCGCCACCTCTAGCAAAATAGTCCCAAGTCTGCAAACTGCAAAACAGAGCTGG 2700
2641 AACTTCGCCACCTCTAGCAAAATAGTCCCAAGTCTGCAAACTGCAAAACAGAGCTGG 2700
2701 CACAGAGGAGGAGGAGCCCTCCAAAAATACGGCAGAGAAATACAAATGAGACGAGAAATTA 2760
2701 CACAGAGGAGGAGGAGCCCTCCAAAAATACGGCAGAGAAATACAAATGAGACGAGAAATTA 2760
2761 CGGTGGAGCTAAGTAGCAAGGATTTCTGGAAAACTGGCATCCGTTCTGTGTCAGC 2820

2761 CGGTGGAGCTAAGTAGCAAGGATTTCTGGAAAACTGGCATCCGTTCTGTGTCAGC 2820
2821 ATGCAATGATGCTACCTGTTCTGACCCCATCATATCCCTACCAAAATGCTTAATGCATT 2880
2821 ATGCAATGATGCTACCTGTTCTGACCCCATCATATCCCTACCAAAATGCTTAATGCATT 2880
2881 TGGACAAGTTGATAGGATATATCTTCCAGATCGTTGCTGTTGACGCTGGCCATGACTC 2940
2881 TGGACAAGTTGATAGGATATATCTTCCAGATCGTTGCTGTTGACGCTGGCCATGACTC 2940
2941 ATCCAAGTCAATCAATTTAAATTTTGGAAATGAATCTGATCATGCGAGAAATCAATATCTA 3000
2941 ATCCAAGTCAATCAATTTAAATTTTGGAAATGAATCTGATCATGCGAGAAATCAATATCTA 3000
3001 ACTGTGGAATTTCCGACGCCCAATATGAGAGACAGAAAGTTTCATCAATGCACATGCGGA 3060
3001 ACTGTGGAATTTCCGACGCCCAATATGAGAGACAGAAAGTTTCATCAATGCACATGCGGA 3060
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3121 CCTCGAGGATTAACCAATGAACGTTGGAAATCTTGGGCTGATGCTGTTGTTGAATTC 3180
3121 CCTCGAGGATTAACCAATGAACGTTGGAAATCTTGGGCTGATGCTGTTGTTGAATTC 3180
3181 TGACCAAGCTTCAATTTGTACTATTTGTTTCTTCTAGTCTGGAAGAGGAGGATTAACCACT 3240
3181 TGACCAAGCTTCAATTTGTACTATTTGTTTCTTCTAGTCTGGAAGAGGAGGATTAACCACT 3240
3241 ATCGGATGTCATTTTTCAGAAATCAGCACTTCCATGCTAGCAAAAGAACTTGAACCTG 3300
3241 ATCGGATGTCATTTTTCAGAAATCAGCACTTCCATGCTAGCAAAAGAACTTGAACCTG 3300
3301 ATCCATTTATGCTGATGCTCAGCGGCTGACCTTTGTAGAGAAATCGGACCTTCGACATG 3360
3301 ATCCATTTATGCTGATGCTCAGCGGCTGACCTTTGTAGAGAAATCGGACCTTCGACATG 3360
3361 CAATGCGCAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTTGGAGGAGGAGCTTGAGG 3420
3361 CAATGCGCAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTTGGAGGAGGAGCTTGAGG 3420
3421 AAGCCAAAGCAGTTTATTTGAGCGCTTCTTAAATGATCCGAGCTTCGCGGAGAGTCTGGC 3480
3421 AAGCCAAAGCAGTTTATTTGAGCGCTTCTTAAATGATCCGAGCTTCGCGGAGAGTCTGGC 3480
3481 TCAATTTATCTCTCCACCCACTCCAACTCAAGAGCCAAATACCTGATCGACAACTTATG 3540
3481 TCAATTTATCTCTCCACCCACTCCAACTCAAGAGCCAAATACCTGATCGACAACTTATG 3540
3541 AAACTTTCTCCAGTTCTACAAAACTTTACTGAGTTTGAAGAGCAATTTGGAGTAAATTTTA 3600
3541 AAACTTTCTCCAGTTCTACAAAACTTTACTGAGTTTGAAGAGCAATTTGGAGTAAATTTTA 3600
3601 CTCAATGTCGACTTCTGGCAAGGGCATTCACATTTGAGAACTGTTGGGATTTAACCATCTGA 3660
3601 CTCAATGTCGACTTCTGGCAAGGGCATTCACATTTGAGAACTGTTGGGATTTAACCATCTGA 3660
3661 CCTTAGGCCACATCAGAGAAATGGAATTTCTAGTGAATCTCAATATGCAACTGGTAGCCA 3720
3661 CCTTAGGCCACATCAGAGAAATGGAATTTCTAGTGAATCTCAATATGCAACTGGTAGCCA 3720
3721 CAGAGTACTTATTTCAATTTCTCCAGATCATCAATGAAGGACACTTAACTTTGTCGAA 3780
3721 CAGAGTACTTATTTCAATTTCTCCAGATCATCAATGAAGGACACTTAACTTTGTCGAA 3780
3781 GCTCTTTGTGTAATATAGAACTCAGGCCAAAGTACGGAGGAGCTGGGATGTCAGAGT 3840
3781 GCTCTTTGTGTAATATAGAACTCAGGCCAAAGTACGGAGGAGCTGGGATGTCAGAGT 3840
3841 AGCCCAATACCAACGACAGAAACCAAGGCTTGTGGCTTCCGACCAAGACCTTGGCG 3900

D	b		3841	ACGCCATAACCAACGACAAGCCAAAGGGCCTGTGGCGCTTCCGACAAGAACCCTTGCGGG	3900
Q	y		3901	ACCTTTTGGGAATCATTTATTTCAGCGCTGTACTCATTAAGAGATTTGGAAATATGTTTCATA	3960
D	b		3901		
D	b		3901	ACCTTTTGGGAATCATTTATTTCAGCGCTGTACTCATTAAGAGATTTGGAAATATGTTTCATA	3960
Q	y		3961	CTTTTCATGAATGCTGCTTCTTTTCCAGATTGGAAGAAATTCATTTTGAATCAGGATTTGGA	4020
D	b		3961	CTTTTCATGAATGCTGCTTCTTTTCCAGATTGGAAGAAATTCATTTTGAATCAGGATTTGGA	4020
Q	y		4021	ATGACCCCCAATCCCAGCTTTCAGCAGTGTTGCTTGACACTTAGGACAGAGAGAAAAAGAGC	4080
D	b		4021	ATGACCCCCAATCCCAGCTTTCAGCAGTGTTGCTTGACACTTAGGACAGAGAGAAAAAGAGC	4080
Q	y		4081	CAGACATTCCTCTGTACAAAGACTCTGCAGACAGTGGGCCCATCCCATGCCGCCGAACCTTACA	4140
D	b		4081	CAGACATTCCTCTGTACAAAGACTCTGCAGACAGTGGGCCCATCCCATGCCGCCGAACCTTACA	4140
Q	y		4141	CTGTGGCTGTTTTATTTCACGGGAGAAAAGANAATAGCTGTGGGAAAGGCCAAAGTATTTCAGC	4200
D	b		4141	CTGTGGCTGTTTTATTTCACGGGAGAAAAGANAATAGCTGTGGGAAAGGCCAAAGTATTTCAGC	4200
Q	y		4201	AAGCGGAAATGGGGAGCAGCAATGGATGCGCTTGAAAAATATAATTTTCCCCAGATGGCCC	4260
D	b		4201	AAGCGGAAATGGGGAGCAGCAATGGATGCGCTTGAAAAATATAATTTTCCCCAGATGGCCC	4260
Q	y		4261	ATCAGAAGCGGTTCCATCGAACGGGAAGTACAGACAAGAGTTTAAAAAGAAATCAGAGTGGGAAA	4320
D	b		4261	ATCAGAAGCGGTTCCATCGAACGGGAAGTACAGACAAGAGTTTAAAAAGAAATCAGAGTGGGAAA	4320
Q	y		4321	GAGAGCATCAAGAGAGAGAGCCAGATCAGACTGGAAGACATCAAGAAATAAAGGAGGGGCAT	4380
D	b		4321	GAGAGCATCAAGAGAGAGAGCCAGATCAGACTGGAAGACATCAAGAAATAAAGGAGGGGCAT	4380
Q	y		4381	GCAAGTGTGGAGTATTTACTTGTCTCAGTAACTGTGACTGTGTGCTATTTAGACCTTAGCCCT	4440
D	b		4381	GCAAGTGTGGAGTATTTACTTGTCTCAGTAACTGTGACTGTGTGCTATTTAGACCTTAGCCCT	4440
Q	y		4441	AGTTTTCTTCGAGACAATGAACGAAGTGTGCTCATTTGAAATATAAATACAGAGTCAAATCG	4500
D	b		4441	AGTTTTCTTCGAGACAATGAACGAAGTGTGCTCATTTGAAATATAAATACAGAGTCAAATCG	4500
Q	y		4501	CTATTGTGTTTTAATGATCTGTTTTTAGCTGGATGGTCTTTATTAACAAAGTATTAGATT	4560
D	b		4501	CTATTGTGTTTTAATGATCTGTTTTTAGCTGGATGGTCTTTATTAACAAAGTATTAGATT	4560
Q	y		4561	TCTTCTTCTATTAAACGGGAAAACCTTGACTTGGTGAATGTGCATTTACTTCTTTTATTTTTG	4620
D	b		4561	TCTTCTTCTATTAAACGGGAAAACCTTGACTTGGTGAATGTGCATTTACTTCTTTTATTTTTG	4620
Q	y		4621	CTCTTTTAAATAATAAAATTCAGAAGGCATATTTCTATGTGGAAATAGATCCCTGTTTTTCCAT	4680
D	b		4621	CTCTTTTAAATAATAAAATTCAGAAGGCATATTTCTATGTGGAAATAGATCCCTGTTTTTCCAT	4680
Q	y		4681	CTGTGTCCTCCAGATTGTGACCCCTAGACTTTTCAATTTGACAAGTAAAAAAATTTGACTTTACTAG	4740
D	b		4691	CTGTGTCCTCCAGATTGTGACCCCTAGACTTTTCAATTTGACAAGTAAAAAAATTTGACTTTACTAG	4740
Q	y		4741	TAAAAAIAAAAAAAAAAAAAAAAAAAAAA 4764	
D	b		4741	TAAAAAIAAAAAAAAAAAAAAAAAAAAAA 4764	

RESULT 8
US-10-723-860-5003
; Sequence 5003, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

781 QY CTCCTCAGTTTAAAGTATTCAGAACCAACCTAGTCTCTTCTGCTCCAGTCTTAATAACA 840
881 Db CTCCTCAGTTTAAAGTATTCAGAACCAACCTAGTCTCTTCTGCTCCAGTCTTAATAACA 940
841 QY GCAGTAGTCTCTCAATTTTCAGAGCATCTCCCTCCATACCCACCTCCCAAGAGCTCCCAAGTGA 900
941 Db GCAGTAGTCTCTCAATTTTCAGAGCATCTCCCTCCATACCCACCTCCCAAGAGCTCCCAAGTGA 1000
901 QY GAAGGTCCCAAGAGCTGAAACACTATGATGACCAAGGACCGAGACCAAGTCAATG 960
1001 Db GAAGGTCCCAAGAGCTGAAACACTATGATGACCAAGGACCGAGACCAAGTCAATG 1060
961 QY GCGAGGTGAGAGCATCTCGTCCCTGATCGCGGGAGCGAGCGCGAGTCCCGACAGGA 1020
1061 Db GCGAGGTGAGAGCATCTCGTCCCTGATCGCGGGAGCGAGCGCGAGTCCCGACAGGA 1120
1021 QY GAAGACAAGACAGCGCGTACAGATCTGATTAATGACCGAGGGAGAACCACTCTCGCCACC 1080
1121 Db GAAGACAAGACAGCGCGTACAGATCTGATTAATGACCGAGGGAGAACCACTCTCGCCACC 1180
1081 QY GCAGCTACGAACCGAGCAGAGAGGAGAAACCGGAGAGACACAGGCACTCGAGAACCGAA 1140
1181 Db GCAGCTACGAACCGAGCAGAGAGGAGAAACCGGAGAGACACAGGCACTCGAGAACCGAA 1240
1141 QY GATCACCATCTCTGGAAGGTCTTACAAAGAGGTATATAGATCTGGAAGGATTAACG 1200
1241 Db GATCACCATCTCTGGAAGGTCTTACAAAGAGGTATATAGATCTGGAAGGATTAACG 1300
1201 QY GTTTATCGGTGTCTCTGAACTCTGATGATGACACAGAGAAATACCTGGGGAGATTAATTA 1260
1301 Db GTTTATCGGTGTCTCTGAACTCTGATGATGACACAGAGAAATACCTGGGGAGATTAATTA 1360
1261 QY AAAATACAGATTTCTGGGCCCCACCTCTGAGATTTGGAATCATTCGCTCCCAAGTAGGG 1320
1361 Db AAAATACAGATTTCTGGGCCCCACCTCTGAGATTTGGAATCATTCGCTCCCAAGTAGGG 1420
1321 QY AGAAGAGAGAGCTCGTTGGGAGGAGAAAGACCGTGGAGTGACACAGAGTCTG 1380
1421 Db AGAAGAGAGAGCTCGTTGGGAGGAGAAAGACCGTGGAGTGACACAGAGTCTG 1480
1381 QY GCAAAGCAAGAACTATACCTCAATCAAGGAAAGAGCCGAGGAGACCATCCCTGACA 1440
1481 Db GCAAAGCAAGAACTATACCTCAATCAAGGAAAGAGCCGAGGAGACCATCCCTGACA 1540
1441 QY AGAATGAGGAGGAGAAAGAACTCTTAAAGCCTGTGTGATTCGATGCACTCATTTAG 1500
1541 Db AGAATGAGGAGGAGAAAGAACTCTTAAAGCCTGTGTGATTCGATGCACTCATTTAG 1600
1501 QY AAAAATCTACTCTCAGTACCCCATGGATCAGTGGGAGATTTCTACAGTGGTTGGAACGA 1560
1601 Db AAAAATCTACTCTCAGTACCCCATGGATCAGTGGGAGATTTCTACAGTGGTTGGAACGA 1660
1561 QY GTAGGCTTCTGTACTTATATGACAAATTTGAGGAGGAGTTGGGGAGCAGGCAAGAAAGG 1620
1661 Db GTAGGCTTCTGTACTTATATGACAAATTTGAGGAGGAGTTGGGGAGCAGGCAAGAAAGG 1720
1621 QY CCAAAGCTCTCGGCTCCGTGGGAAACCTTCAAAGACGAAGCTCGATGAAGATTTAGAGA 1680
1721 Db CCAAAGCTCTCGGCTCCGTGGGAAACCTTCAAAGACGAAGCTCGATGAAGATTTAGAGA 1780
1681 QY GTTCCAGTGAATCCGAGTGTAGTCTGATGAGACACGACCTGTTCTAGAGCTCAGACT 1740
1781 Db GTTCCAGTGAATCCGAGTGTAGTCTGATGAGACACGACCTGTTCTAGAGCTCAGACT 1840
1741 QY CTGAGTCTTTGAGCTTATTTGAGAAATCAAAACGCAAAAGGCCACCTGACCGACTTC 1800
1841 Db CTGAGTCTTTGAGCTTATTTGAGAAATCAAAACGCAAAAGGCCACCTGACCGCTTCA 1900
1801 QY ATGATGAATCTTGGTACACGATCCAGGCGCAGATGAATGATGACCACTCTGCAATGCA 1860
1901 Db A--AGGAATCTTGGTACACGATCCAGGCGCAGATGAATGATGACCACTCTGCAATGCA 1958
1861 QY GCGCAAGGCAAGACGACAGGAATTTAGGACAGCAATTTATCTCTGGAGAGAGGCCATCA 1920

1959 Db GCGCAAGGCAAGACGACAGGAATTTAGGCACAGCATTTATCTTGGAGAGAGGCCATCA 2018
1921 QY AGCCCTGTCTCTCTATGACCAACAAATGCTGGCAGACTTTTCCACTACCGGATCACAGTCT 1980
2019 Db AGCCCTGTCTCTCTATGACCAACAAATGCTGGCAGACTTTTCCACTACCGGATCACAGTCT 2078
1981 QY CCGCGCTCTAGCAACTTTTAACTGACAGGCGCACTGTTATAGAAATACGATGATCACAGT 2040
2079 Db CCGCGCTCTAGCAACTTTTAACTGACAGGCGCACTGTTATAGAAATACGATGATCACAGT 2138
2041 QY ATATCTTTGAAGGATTTCTATGTTGCAATGCCCCCTGACCAATATTTCCACTGTGTA 2100
2139 Db ATATCTTTGAAGGATTTCTATGTTGCAATGCCCCCTGACCAATATTTCCACTGTGTA 2198
2101 QY AAGTAAATTAGATTCAACATAGACTACACGATTTCAATTTTGAAGAGATGATGCGGAGA 2160
2199 Db AAGTAAATTAGATTCAACATAGACTACACGATTTCAATTTTGAAGAGATGATGCGGAGA 2258
2161 QY ATTTTGTGTGAAAGGCTTTGAACTCTTTTCACTGTTCTTATTCAGAGATATTTTGAAT 2220
2259 Db ATTTTGTGTGAAAGGCTTTGAACTCTTTTCACTGTTCTTATTCAGAGATATTTTGAAT 2318
2221 QY TATATGACTGGAATCTTAAAGGTCTTTGTTTGAAGACAGCCCTCCCTGCTGCCCAAGAT 2280
2319 Db TATATGACTGGAATCTTAAAGGTCTTTGTTTGAAGACAGCCCTCCCTGCTGCCCAAGAT 2378
2281 QY TTTCAATTCATGCCACGTTTGTAAAGATTTCTCCAGATGAGGAAAGAAAGTGTCTCCA 2340
2379 Db TTTCAATTCATGCCACGTTTGTAAAGATTTCTCCAGATGAGGAAAGAAAGTGTCTCCA 2438
2341 QY TGCAACAGATTTCTCTGTACTTGTAAAGGTGACAGAACCCCTGCTGCTGAGAGAGA 2400
2439 Db TGCAACAGATTTCTCTGTACTTGTAAAGGTGACAGAACCCCTGCTGCTGAGAGAGA 2498
2401 QY TTTGCCAATATGCTTCAAGTGGAGGCTGGAGTGGCAGAAATATGCAAGAAATGCAAG 2460
2499 Db TTTGCCAATATGCTTCAAGTGGAGGCTGGAGTGGCAGAAATATGCAAGAAATGCAAG 2558
2461 QY GCATGATTTGTACCAACCCCTGGGACGAAACCAAGCTCTGTCCGTATCGATCAACTGATC 2520
2559 Db GCATGATTTGTACCAACCCCTGGGACGAAACCAAGCTCTGTCCGTATCGATCAACTGATC 2618
2521 QY GTGAAACAGTTCAACCCCGATGTGATTTATTTTCCGATTTATCGTCCACTTTGGGATACGCC 2580
2619 Db GTGAAACAGTTCAACCCCGATGTGATTTATTTTCCGATTTATCGTCCACTTTGGGATACGCC 2678
2581 QY CTGCAAGTTGAGTTATGAGGAGACCCACAGTACCAAAACCTGTGGAAGAGTTATGTA 2640
2679 Db CTGCAAGTTGAGTTATGAGGAGACCCACAGTACCAAAACCTGTGGAAGAGTTATGTA 2738
2641 QY AACTTCCGCACTCTCTAGCAAAATAGTCCCAAGTCAAAACCTGCAAAACAGAAAGCTGG 2700
2739 Db AACTTCCGCACTCTCTAGCAAAATAGTCCCAAGTCAAAACCTGCAAAACAGAAAGCTGG 2798
2701 QY CACAGAGGAGAGAGCCCTCCAAAAATACGCGAGAGAAATACAATGAGACGAGAGATA 2760
2799 Db CACAGAGGAGAGAGCCCTCCAAAAATACGCGAGAGAAATACAATGAGACGAGAGATA 2858
2761 QY CGGTGAGCTAAGTAGCCAGGATTTCTGGAACTGCGCATCCGTTCTGATGCTGTGACG 2820
2859 Db CGGTGAGCTAAGTAGCCAGGATTTCTGGAACTGCGCATCCGTTCTGATGCTGTGACG 2918
2821 QY ATGCAATGATGCTTACCTGTTGACCCATCATATCCGCTACCAACCAATGCTTAATGAT 2880
2919 Db ATGCAATGATGCTTACCTGTTGACCCATCATATCCGCTACCAACCAATGCTTAATGAT 2978
2881 QY TGGACAAGTTGATGAGATATCTTTTCAAAGATGCTTGTCTGTTGACGCTGGCCATGACTC 2940
2979 Db TGGACAAGTTGATGAGATATCTTTTCAAAGATGCTTGTCTGTTGACGCTGGCCATGACTC 3038
2941 QY ATCCAAAGTCACTCAATTTAAATTTTGGAAATGAAATCTGATCATGCGCAAGAAATTCATTA 3000

Db	3039	ATCCAAGTCATCATTTTAAAATTTTGGAAATGAATCCTTGATCATGCCAGGAATTCATTATATCTA	3098
Qy	3001	ACTGTGGAAATTCGGCAGCCCCAAAATACGGAGACAGAAAAGTTCATCACATGCACATGCGGA	3060
Db	3099	ACTGTGGAAATTCGGCAGCCCCAAAATACGGAGACAGAAAAGTTCATCACATGCACATGCGGA	3158
Qy	3061	AGAAAGGGAATTAACACCTTGTATAAATATCATGTACGCTTCGGCCAAAGATGACCAATC	3120
Db	3159	AGAAAGGGAATTAACACCTTGTATAAATATCATGTACGCTTCGGCCAAAGATGACCAATC	3218
Qy	3121	CCTCGAGGATTAACCAACAATGAACGGTTGGAAATTCCTGGTGATGCTGTGTGTGAATTC	3180
Db	3219	CCTCGAGGATTAACCAACAATGAACGGTTGGAAATTCCTGGTGATGCTGTGTGTGAATTC	3278
Qy	3181	TGACACGGTCCATTTGCTACTATTTGTTTCTAGTCTGGAAGAAAGGAGGATTAGCAACT	3240
Db	3279	TGACACGGTCCATTTGCTACTATTTGTTTCTAGTCTGGAAGAAAGGAGGATTAGCAACT	3338
Qy	3241	ATCCGACTGCCATTTGTTCAGAATCAGCACCTTGCCATGCTAGCAAGAAACCTTGAACCTG	3300
Db	3339	ATCCGACTGCCATTTGTTCAGAATCAGCACCTTGCCATGCTAGCAAGAAACCTTGAACCTG	3398
Qy	3301	ATCCATTTATGCTGTATGCTCA CGGGCTGACCTTTGTAGAGNATCGGACCTTCGCATG	3360
Db	3399	ATCCATTTATGCTGTATGCTCA CGGGCTGACCTTTGTAGAGNATCGGACCTTCGCATG	3458
Qy	3361	CAATGGCCAAATGTGTTTGAACGTTAATAGAGCTGTTTACTTTGAGGGAAGCCTGGAGG	3420
Db	3459	CAATGGCCAAATGTGTTTGAACGTTAATAGAGCTGTTTACTTTGAGGGAAGCCTGGAGG	3518
Qy	3421	AAGCCAAAGCAGTTATTTGGACGCTTGCTTTTAAATGATCCGACCTTCGCGGAAGTCTGCG	3480
Db	3519	AAGCCAAAGCAGTTATTTGGACGCTTGCTTTTAAATGATCCGACCTTCGCGGAAGTCTGCG	3578
Qy	3481	TCAATATATCTCTCA CCCCCTCAACAACAATGATGATCGGACCAATATGATCGGACACTTATG	3540
Db	3579	TCAATATATCTCTCA CCCCCTCAACAACAATGATGATCGGACCAATATGATCGGACACTTATG	3638
Qy	3541	AAACTTCTCCAGTTCTCAAAAACTTACTGAGTTTGAAGAACAAATGAGAGTAATTTTAA	3600
Db	3639	AAACTTCTCCAGTTCTCAAAAACTTACTGAGTTTGAAGAACAAATGAGAGTAATTTTAA	3698
Qy	3601	CTCATGTTTCGACTTCTGCGAAGGCATTCACATTTAGAACTGTGGGATTTAAACATCTGA	3660
Db	3699	CTCATGTTTCGACTTCTGCGAAGGCATTCACATTTAGAACTGTGGGATTTAAACATCTGA	3758
Qy	3661	CCCTAGGCCCAATACAGAGAAATGGAATTCCTAGTGTACTCATTAATGCAACTCGTAGCCCA	3720
Db	3759	CCCTAGGCCCAATACAGAGAAATGGAATTCCTAGTGTACTCATTAATGCAACTCGTAGCCCA	3818
Qy	3721	CAGAGTACTTATTTCAATTTCCAGATCATCATGAAGGACACTTAACTTTGTTCGCA	3780
Db	3819	CAGAGTACTTATTTCAATTTCCAGATCATCATGAAGGACACTTAACTTTGTTCGCA	3878
Qy	3781	GCCTTTTGGTGAATTAATAGAACTCAGGCCAAAGGTAGCGGAGGAGCTGGGCAATGCAGAGT	3840
Db	3879	GCCTTTTGGTGAATTAATAGAACTCAGGCCAAAGGTAGCGGAGGAGCTGGGCAATGCAGAGT	3938
Qy	3841	AGCCCAATACCAACGACAGACCAAGAGCCCTGTGGCGCTTCGCACCAAGACCTTCGCGG	3900
Db	3939	AGCCCAATACCAACGACAGACCAAGAGCCCTGTGGCGCTTCGCACCAAGACCTTCGCGG	3998
Qy	3901	ACCTTTTGGAAATCATTTTATTTGAGCGCTGTACACTGATAAGGATTTGGAATATGTTTCA	3960
Db	3999	ACCTTTTGGAAATCATTTTATTTGAGCGCTGTACACTGATAAGGATTTGGAATATGTTTCA	4058
Qy	3961	CTTTTCATGAATGTCTGCTTTCTTTCCACGATTTGAAAGAAATTCATTTTGAATCAGAGTTGGA	4020
Db	4059	CTTTTCATGAATGTCTGCTTTCTTTCCACGATTTGAAAGAAATTCATTTTGAATCAGAGTTGGA	4118
Qy	4021	ATGACCCCAAAATCCCGACTTCAGCAGTGTGCTTCACACTTAGGACAGAGGAAAGAGC	4080
Db	4119	ATGACCCCAAAATCCCGACTTCAGCAGTGTGCTTCACACTTAGGACAGAGGAAAGAGC	4178

RESULT 9	APPLI	LENG
US-10-20	APPLI	TYPE
; Sequen	APPLI	ORGR
; Public	APPLI	FEAR
; GENERA	APPLI	
; APPLI	FILE	
; APPLI	CURR	
; APPLI	CURR	
; APPLI	PRIOR	
; APPLI	PRIOR	
; TITLE	NUMB	
; FILE	SOFT	
; CURR	SEQ II	
; CURR		
; PRIOR		
; PRIOR		
; NUMB		
; SOFT		
; SEQ II		
; LENG		
; TYPE		
; ORGR		
; FEAR		

OTHER INFORMATION: Putative ribonuclease III
US-10-205-331-117

Query Match 34.0%; Score 1619.6; DB 7; Length 1626;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1622; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	2745	ATGAGAGGAGAGTAACGGTGGAGCTAAGTAGCCCAAGGATCTCGGAAATCTGGGATCGGT	2804
Db	1	ATGAGAGGAGAGTAACGGTGGAGCTAAGTAGCCCAAGGATCTCGGAAATCTGGGATCGGT	60
Qy	2805	TCTGATCTCTGTCAGCATGCAATGATGCTACTCTCTGACCCCATCATATCCGCTACAC	2864
Db	61	TCTGATCTCTGTCAGCATGCAATGATGCTACTCTCTGACCCCATCATATCCGCTACAC	120
Qy	2865	CAATGCCATATGCAATTTGGCAAGTTGATAGGATATCTTTTCAAGATCGTGTCTGTG	2924
Db	121	CAATGCCATATGCAATTTGGCAAGTTGATAGGATATCTTTTCAAGATCGTGTCTGTG	180
Qy	2925	CAGTGGCCATGACTCATCCAGTCATCTTAATTTTGGATGATCTCTGATCATGCC	2984
Db	181	CAGTGGCCATGACTCATCCAGTCATCTTAATTTTGGATGATCTCTGATCATGCC	240
Qy	2985	AGGAATTCATTTCTAACTCTGGAATTCGGCAGCCCAATACCGAGACAGAAAGTTTCA	3044
Db	241	AGGAATTCATTTCTAACTCTGGAATTCGGCAGCCCAATACCGAGACAGAAAGTTTCA	300
Qy	3045	CACATGACATGCGGAAGGAAGGATTAACACCTTGTATTAATATCATGTCAACGCTTGGC	3104
Db	301	CACATGACATGCGGAAGGAAGGATTAACACCTTGTATTAATATCATGTCAACGCTTGGC	360
Qy	3105	CAAGATGACCACTCCCTCGAGGATTAACACCAATGAACGGTTGGAATTCCTGGGTGAT	3164
Db	361	CAAGATGACCACTCCCTCGAGGATTAACACCAATGAACGGTTGGAATTCCTGGGTGAT	420
Qy	3165	GCTGTTGTTGAAATTTCTGACAGCGTCCATTTGTACTATTTTCTCTAGTCTGGAAGAA	3224
Db	421	GCTGTTGTTGAAATTTCTGACAGCGTCCATTTGTACTATTTTCTCTAGTCTGGAAGAA	480
Qy	3225	GGAGGATTAGCAACCTATCGGACTGCCATTTGTCAGAAATCAGCACCTTGCCTAGCA	3284
Db	481	GGAGGATTAGCAACCTATCGGACTGCCATTTGTCAGAAATCAGCACCTTGCCTAGCA	540
Qy	3285	AAGAACTTGAATCTGATGATTTATGCTGATGCTCAGCGGCTGACCTTTGTAGAGAA	3344
Db	541	AAGAACTTGAATCTGATGATTTATGCTGATGCTCAGCGGCTGACCTTTGTAGAGAA	600
Qy	3345	TCGGACCTTCGACATGCAATGGCCAAATTTGTAAGCGTTAATAGGAGCTGTTTACTTG	3404
Db	601	TCGGACCTTCGACATGCAATGGCCAAATTTGTAAGCGTTAATAGGAGCTGTTTACTTG	660
Qy	3405	GAGGGAAGCTCGGAGGAAGCAAGCAGTTAATTTGGAGCGTTGCTCTTTAATGATCCGGAC	3464
Db	661	GAGGGAAGCTCGGAGGAAGCAAGCAGTTAATTTGGAGCGTTGCTCTTTAATGATCCGGAC	720
Qy	3465	CTCGGGAAGTCTGGCTCAATTAATCTCTCCACCCACTCAACTACAGAGCAAAATACT	3524
Db	721	CTCGGGAAGTCTGGCTCAATTAATCTCTCCACCCACTCAACTACAGAGCAAAATACT	780
Qy	3525	GATCGACAACTTAATGAACTCTCAGTTCTCAAAATCTTACTGAGTTTGAAGAGCA	3584
Db	781	GATCGACAACTTAATGAACTCTCAGTTCTCAAAATCTTACTGAGTTTGAAGAGCA	840
Qy	3585	ATTGGAGTAATTTTACTCATGTTTCCGACTCTCGGCAAGGCAATTCATTTGAGAACTGTG	3644
Db	841	ATTGGAGTAATTTTACTCATGTTTCCGACTCTCGGCAAGGCAATTCATTTGAGAACTGTG	900
Qy	3645	GGATTTAAACATCTGACCCCTAGGCCCAATACAGAGAAATGGAATTCCTAGGTGACTCATA	3704
Db	901	GGATTTAAACATCTGACCCCTAGGCCCAATACAGAGAAATGGAATTCCTAGGTGACTCATA	960
Qy	3705	ATGCAATCTGTAGCCACAGAGTACTTATTCATTTCCAGATCATCATGAGGACAC	3764

Db	961	ATGCAACTGTGTAGCCACAGAGTACTTATTATTCCAGATCATCATGAGGACAC	1020
Qy	3765	TTAACTTTGTGGCAAGCTCTTTGGTGAATAATAAGAACTCAGGCCAAGGTAGCGGAGAG	3824
Db	1021	TTAACTTTGTGGCAAGCTCTTTGGTGAATAATAAGAACTCAGGCCAAGGTAGCGGAGAG	1080
Qy	3825	CTGGCATGCAAGGATGAGCCATTAACCAACGACCAAGACCAAGAGGCTGTGGCGCTTCGC	3884
Db	1081	CTGGCATGCAAGGATGAGCCATTAACCAACGACCAAGACCAAGAGGCTGTGGCGCTTCGC	1140
Qy	3885	ACCAAGACCTTTGGCGGACCTTTTGGGAATCATTTATTGACGCGCTGTACACTGATAAGGAT	3944
Db	1141	ACCAAGACCTTTGGCGGACCTTTTGGGAATCATTTATTGACGCGCTGTACACTGATAAGGAT	1200
Qy	3945	TTGGAATATGTTCTATCTTTCTTCAATGATGTCTCTTCTTCCACCAATTTGAAAGAAATTCATT	4004
Db	1201	TTGGAATATGTTCTATCTTTCTTCAATGATGTCTCTTCTTCCACCAATTTGAAAGAAATTCATT	1260
Qy	4005	TTGGAATCAGGATTTGGGAATGACCCCAATCCAGCTTCAGCAGTGTCTTGCACACTTAGG	4064
Db	1261	TTGGAATCAGGATTTGGGAATGACCCCAATCCAGCTTCAGCAGTGTCTTGCACACTTAGG	1320
Qy	4065	ACAGAGGAAAAGAGCCAGACATTTCTCTGTACAAAGACTCTGACAGACAGTGGGCCCATCC	4124
Db	1321	ACAGAGGAAAAGAGCCAGACATTTCTCTGTACAAAGACTCTGACAGACAGTGGGCCCATCC	1380
Qy	4125	CATGCCGAAACCTACACTGTGGCTGTTTATTTTCAAGGAGAAAGAAATAGGCTGTGGGAAA	4184
Db	1381	CATGCCGAAACCTACACTGTGGCTGTTTATTTTCAAGGAGAAAGAAATAGGCTGTGGGAAA	1440
Qy	4185	GGACCAAGTATTCAGCAACGGGAATGGGAGCAGCAATGCGCTTGAATAATATTAAT	4244
Db	1441	GGACCAAGTATTCAGCAACGGGAATGGGAGCAGCAATGCGCTTGAATAATATTAAT	1500
Qy	4245	TTTCCCAGATGCGCCCATCAGAAAGCGTTTCATCGAACGGAAGTACAGACAGAGTTAAAA	4304
Db	1501	TTTCCCAGATGCGCCCATCAGAAAGCGTTTCATCGAACGGAAGTACAGACAGAGTTAAAA	1560
Qy	4305	GAAATGAGGTGGGAAAAGAGAGCATCAAGAGAGAGCCAGATGAGACTGAAAGACATCAAG	4364
Db	1561	GAAATGAGGTGGGAAAAGAGAGCATCAAGAGAGAGCCAGATGAGACTGAAAGACATCAAG	1620
Qy	4365	AAATAA 4370	
Db	1621	AAATNA 1626	

RESULT 10
US-10-313-313-23
; Sequence 23, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ07C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-313-23

Query Match 29.4%; Score 1398.6; DB 5; Length 1458;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1412; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
Qy 3234 GCACCTATCGGACTGCCATTTGTTCAAGAAATCAGACCTTGCCTAGCAAGAACTT 3293
Db 24 GCACCTATCGGACTGCCATTTGTTCAAGAAATCAGACCTTGCCTAGCAAGAACTT 83

QY	3294	GAACCTGGATCCCAATTTATGCTGTATGCTCAGCGGCTTGACCTTTGTATAGAAATCGGACCTTT	3353
Db	84	GAACCTGGATCGAATTTATGCTGTATGCTCAGCGGCTTGACCTTTGTATAGAAATCGGACCTTT	143
QY	3354	CGACATGCAATGGCCAAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTTGGAGGAAGC	3413
Db	144	CGACATGCAATGGCCAAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTTGGAGGAAGC	203
QY	3414	CTGGAGGAAGCCAAAGCAGTTATTTGGACGCTTGCTCTTTAATGATCCGACCTGCGCGAA	3473
Db	204	CTGGAGGAAGCCAAAGCAGTTATTTGGACGCTTGCTCTTTAATGATCCGACCTGCGCGAA	263
QY	3474	GTCTGGCTCAATTTATCTCTCCACCACTCCAACTACAAGAGCCAAATACTGATCGACAA	3533
Db	264	GTCTGGCTCAATTTATCTCTCCACCACTCCAACTACAAGAGCCAAATACTGATCGACAA	323
QY	3534	CTTATTTGAACCTTCTCAGTTCTACAAAATTTACTGAGTTTCAAGAGCAATTTGGAGTA	3593
Db	324	CTTATTTGAACCTTCTCAGTTCTACAAAATTTACTGAGTTTCAAGAGCAATTTGGAGTA	383
QY	3594	ATTTTACTCATGTTCTGACCTTCTGGCAAGGCGAATTCACATTTGAGAACTGTGGATTTAAC	3653
Db	384	ATTTTACTCATG-TGACCTTCTGGCAAGGCGAATTCACATTTGAGAACTGTGGATTTAAC	442
QY	3654	CATCTGACCTTAGGCCCAATCAGAGAAATGGAATTCCTAGGTGACTCCATAATGCAACTG	3713
Db	443	CATCTGACCTTAGGCCCAATCAGAGAAATGGAATTCCTAGGTGACTCCATAATGCAACTG	502
QY	3714	GTAGCCACAGAGTACTTATTCATTTCCAGATCATCATGAGGACACTTAACTTTG	3773
Db	503	GTAGCCACAGAGTACTTATTCATTTCCAGATCATCATGAGGACACTTAACTTTG	562
QY	3774	TTGGGAGCTCTTTGGTGAATATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGGCATG	3833
Db	563	TTGGGAGCTCTTTGGTGAATATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGGCATG	622
QY	3834	CAGGAGTACGCCATAACCAACGACGACCAAGAGGCGCTGTGGCGCTTCGCACCAAGCC	3893
Db	623	CAGGAGTACGCCATAACCAACGACGACCAAGAGGCGCTGTGGCGCTTCGCACCAAGCC	682
QY	3894	TTGGCGGACCTTTTGGAAATCATTTATTTGCGCGCTGTACACTGATAGGATTTGGAATAT	3953
Db	683	TTGGCGGACCTTTTGGAAATCATTTATTTGCGCGCTGTACACTGATAGGATTTGGAATAT	742
QY	3954	GTTTCATCTTTTCATGAATGCTGCTCTTTCCAGATTGAAAGAAATTCATTTTGAATCAG	4013
Db	743	GTTTCATCTTTTCATGAATGCTGCTCTTTCCAGATTGAAAGAAATTCATTTTGAATCAG	802
QY	4014	GATTTGGAATGACCCCAATCCAGCTTCAGCAGTGTGCTTTGACACTTTAGGACAGAAGGA	4073
Db	803	GATTTGGAATGACCCCAATCCAGCTTCAGCAGTGTGCTTTGACACTTTAGGACAGAAGGA	862
QY	4074	AAAGAGCCAGACATTCCTCTGTACAAGACTCTGACAGTGGGCCCATCCATGCCCCGA	4133
Db	863	AAAGAGCCAGACATTCCTCTGTACAAGACTCTGACAGTGGGCCCATCCATGCCCCGA	922
QY	4134	ACCTACACTGTGCGCTGTTTATTTCAAGGGAGAAAGATPAGGCTGTGGGAAAGGACCAAGT	4193
Db	923	ACCTACACTGTGCGCTGTTTATTTCAAGGGAGAAAGATPAGGCTGTGGGAAAGGACCAAGT	982
QY	4194	ATTGAGCAAGCGGAAATGGGAGCAGCAATGGATGCGCTTTGAAAAATATAATTTTCCCAG	4253
Db	983	ATTGAGCAAGCGGAAATGGGAGCAGCAATGGATGCGCTTTGAAAAATATAATTTTCCCAG	1042
QY	4254	ATGCCCCATCAGAGCGGTTTCATCGAACGGAAGTTACAGACAGAGTTTAAAGAAATGAGG	4313
Db	1043	ATGCCCCATCAGAGCGGTTTCATCGAACGGAAGTTACAGACAGAGTTTAAAGAAATGAGG	1102
QY	4314	TGGGAAAGAGAGCATCAAGAGAGAGGACCATGAGTGAAGCATCAAGAAATAAAGG	4373
Db	1103	TGGGAAAGAGAGCATCAAGAGAGAGGACCATGAGTGAAGCATCAAGAAATAAAGG	1162

QY	4374	AGGGCATGCAAGTGTGGAGTATTTACTTGCTCAGTAACCTGTGACTGTTGCTTATTGAGAC	4433
Db	1163	AGGGCATGCAAGTGTGGAGTATTTACTTGCTCAGTAACCTGTGACTGTTGCTTATTGAGAC	1222
QY	4434	CTAGCCTAGTCTTTTCTGCGACACAATGAAAGTGTCTCATTTGAAATAAATAACAGAGT	4493
Db	1223	CTAGCCTAGTCTTTTCTGCGACACAATGAAAGTGTCTCATTTGAAATAAATAACAGAGT	1282
QY	4494	CAAAATCGCTATTGTTGTTTTTAATGATCTGTTTTAGCTCGATGCTCTTTATTACAAAGTA	4553
Db	1283	CAAAATCGCTATTGTTGTTTTTAATGATCTGTTTTAGCTCGATGCTCTTTATTACAAAGTA	1342
QY	4554	TTAGATTTTCTCTCTATTTAAACGGAAACTTGCATTTGTGTAATGTGCTTACTTCTTT	4613
Db	1343	TTAGATTTTCTCTCTATTTAAACGGAAACTTGCATTTGTGTAATGTGCTTACTTCTTT	1402
QY	4614	TATTTTGTCTCTTTTAAATAATAAATTTCAAGAGCATA	4650
Db	1403	TATTTTGTCTCTTTTAAATAATAAATTTCAAGAGCATA	1439

RESULT 11

US-10-103-313-187

; Sequence 187, Application US/10103313

; Publication No. US20030082758A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PJZ07C1

; CURRENT APPLICATION NUMBER: US/10/103,313

; CURRENT FILING DATE: 2002-03-12

; NUMBER OF SEQ ID NOS: 653

; Prior Application removed - See File Wrapper or Palm

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 187

; LENGTH: 1314

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-103-313-187

Query Match 26.5%; Score 1262.4; DB 5; Length 1314;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1263; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY	3234	GCAACCTATCGGACTGCCATTTGTTTCAAGATCAGCACCTTGCATGCTAGCAAGAACTT	61
Db	2	GCAACCTATCGGACTGCCATTTGTTTCAAGATCAGCACCTTGCATGCTAGCAAGAACTT	61
QY	3294	GAACTGGATCCATTTATGCTGTATGCTCAGGGGCTGACCTTTGTAGAGAAATCGGACCTT	3353
Db	62	GAACTGGATCCATTTATGCTGTATGCTCAGGGGCTGACCTTTGTAGAGAAATCGGACCTT	121
QY	3354	CGACATCAATGGCCAAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTTGGAGGAAGC	181
Db	122	CGACATCAATGGCCAAATTTGTTTGAAGCGTTAATAGGAGCTGTTTACTTTGGAGGAAGC	181
QY	3414	CTGAGAGAGCCAAAGCAGTTATTTGGAGCGCTGCTCTTTAATGATCCGACCTCGCGAA	3473
Db	182	CTGAGAGAGCCAAAGCAGTTATTTGGAGCGCTGCTCTTTAATGATCCGACCTCGCGAA	241
QY	3474	GTCTGGCTCAATTTATCTCTCCACCACTCCAACTACAAGAGCCAAATACTGATCGACAA	3533
Db	242	GTCTGGCTCAATTTATCTCTCCACCACTCCAACTACAAGAGCCAAATACTGATCGACAA	301
QY	3534	CTTATTTGAAACTTCTCCAGTTCTACAAAACTTACTGAGTTTGAAGAGCAATTTGGAGTA	3593
Db	302	CTTATTTGAAACTTCTCCAGTTCTACAAAACTTACTGAGTTTGAAGAGCAATTTGGAGTA	361
QY	3594	ATTTTACTCATGTTTGCAGCTTCTGCAAGGCGATTCACATTTGAGAACTGTGGATTTAAC	3653
Db	362	ATTTTACTCATGTTTGCAGCTTCTGCAAGGCGATTCACATTTGAGAACTGTGGATTTAAC	421
QY	3654	CATCTGACCTTAGGCCCAATCAGAGAAATGGAATTTCTTAGTGTGACTCCATTAATGCAACTG	3713


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Db 422 CATCTGACCTTAGCCACATCAGAGATGGAATTCCTAGTACTCCATTAATGCACTG 481
Qy 3714 GTAGCCACAGAGTACTTATTCATTCATTTCCAGATCATCATGAAGACACTTAACTTTG 3773
Db 482 GTAGCCACAGAGTACTTATTCATTCATTTCCAGATCATCATGAAGACACTTAACTTTG 541
Qy 3774 TTGCGAAGCTCTTTGGTGAATATAGAACTCAGGCCAAGGTAGCGGAGCTGGGCATG 3833
Db 542 TTGCGAAGCTCTTTGGTGAATATAGAACTCAGGCCAAGGTAGCGGAGCTGGGCATG 601
Qy 3834 CAGAGTAGCCATAACCAACGACAGACCAAGAGGCTGTGGCTTCGCACCAAGACC 3893
Db 602 CAGAGTAGCCATAACCAACGACAGACCAAGAGGCTGTGGCTTCGCACCAAGACC 661
Qy 3894 TTGCGGAGCTTTTGGAACTATTTATTCAGCGCTGTACACTGATGAATTTGGAATAT 3953
Db 662 TTGCGGAGCTTTTGGAACTATTTATTCAGCGCTGTACACTGATGAATTTGGAATAT 721
Qy 3954 GTTCATCTTTCATGAATGCTGCTTTCTTCCACGATTCGAAGATTCATTTGAATCAG 4013
Db 722 GTTCATCTTTCATGAATGCTGCTTTCTTCCACGATTCGAAGATTCATTTGAATCAG 781
Qy 4014 GATTGAATGACCCCAATCCCACTTCAGAGTGTGTTGACACTTAGGACAGAGGA 4073
Db 782 GATTGAATGACCCCAATCCCACTTCAGAGTGTGTTGACACTTAGGACAGAGGA 841
Qy 4074 AAAGAGCCACAGATTCCTCTGTACAAGACTCTGCACAGAGTGGGCCATCCCATGCCGA 4133
Db 842 AAAGAGCCACAGATTCCTCTGTACAAGACTCTGCACAGAGTGGGCCATCCCATGCCGA 901
Qy 4134 ACCTACACTGTGGCTGTTTATTTCAAGGAGAAAGAAATAGGCTGTGGGAAAGACCAAGT 4193
Db 902 ACCTACACTGTGGCTGTTTATTTCAAGGAGAAAGAAATAGGCTGTGGGAAAGACCAAGT 961
Qy 4194 ATTTCAGAGCGGAATGGAGCAGCAATGGATGGCTTGGAAATATATTTTCCCCAG 4253
Db 962 ATTTCAGAGCGGAATGGAGCAGCAATGGATGGCTTGGAAATATATTTTCCCCAG 1021
Qy 4254 ATGGCCCATCAGAAGCGGTTTCATCGAAGGAAGTACAGACAGAGTTAAAGAAATGAGG 4313
Db 1022 ATGGCCCATCAGAAGCGGTTTCATCGAAGGAAGTACAGACAGAGTTAAAGAAATGAGG 1081
Qy 4314 TGGGAAGAGAGCATCAAGAGAGAGAGCCAGATGAGACTGAAGACATCAAGAAATAAAGG 4373
Db 1082 TGGGAAGAGAGCATCAAGAGAGAGAGCCAGATGAGACTGAAGACATCAAGAAATAAAGG 1141
Qy 4374 AGGGATGCAAGTGTGGAGTATTTACTTCTCAGTAACTGTGCTGTTCTATTGAGAC 4433
Db 1142 AGGGATGCAAGTGTGGAGTATTTACTTCTCAGTAACTGTGCTGTTCTATTGAGAC 1201
Qy 4434 CTAGCTAGTTTTCTTCGACAGCAATGAACGAAGTGTGCTCATTTGAATAAATAACAGAGT 4493
Db 1202 CTAGCTAGTTTTCTTCGACAGCAATGAAGTGTGCTCATTTGAATAAATAACAGAGT 1261
Qy 4494 CAAATCGCTA 4503
Db 1262 CAAATCGCAA 1271
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RESULT 12

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US-11-097-143-2408
; Sequence 2408, Application US/11097143
; Publication No. US2005020858A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
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; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2408
; LENGTH: 4275
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-2408
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Query Match 16.2%; Score 770.2; DB 10; Length 4275;
Best Local Similarity 58.2%; Pred. No. 2e-208;
Matches 1489; Conservative 0; Mismatches 1023; Indels 45; Gaps 6;

Qy 1758 ATTGCAGAAATCAAAACGCAAAAGGCCACCTGACCGACTTCATGATGAACCTTGTGATC 1817
Db 1151 ATGGAGGAGCTTTCGGCAAGGTGCAACATCCGACGGTGTGCACCGGATCTCTGGCAC 1210
Qy 1818 AACGATCCAGGCCAGATGAATGATGACCACTCTGCAAAATGCAAGCCAAAGGCAAGACGC 1877
Db 1211 AACGAGCGGTGAGATGAACGACGACCTCTTTGCGCTGTCTACGCAAGTCCCGGCGC 1270
Qy 1878 ACAGAAATTAGGACACAGCAATTTATCTGTGAGAGAGGCCATCAAGCCCTGTGTCCTATG 1937
Db 1271 ATTGGCATTCGACACGGCATATATCCGGCGGAGACTGGCTGATATAAGTTGTGCGATCCAAAC 1330
Qy 1938 ACCAAATATGCTGGCAGACTTTTCCACTACCGATCAGCTCTCCCGGCTACGAACCTT 1997
Db 1331 ACACAAATGCAAGGCAAGCTGTTCCACTACAGATCAGCATCTCACCGCCCACTAATCTC 1390
Qy 1998 TTAACCTGACAGGCCAACTGTTATAGAAATACGATGATCAGAGTATATCTTTGAAGGATTT 2057
Db 1391 CTGACAAAGACACCCCACTTATCAAGCATGATGACACAGTTCCTATTTCGAGGSGCTTC 1450
Qy 2058 TCTATGTTTGACATGCCCCCTGACCAATATTTCCACTGTGTAAAGTAATTAATGATTAAC 2117
Db 1451 TCACCTTCTCTGCAATGTGCTCTCTCCGATCTGCGCGTCTGCAAGGTGATCCGCTTCAAC 1510
Qy 2118 ATAGACTACAGATTCATTTTCATGAAGAGATGATGCGGAGAAATTTTGTGTGAAGGS 2177
Db 1511 ATCGAGTACACATTTAGTACGAAGAGGAGAAAGTGCACAGAACTTCACCATCCACAGAG 1570
Qy 2178 CTTGAACTCTTTTCACTGTTCCTATTTCAGAGATATTTTGGAAATATATGACTGGAACTTT 2237
Db 1571 CTAGACATTTTTTCAAAATACCTGTTTCATGAATCTGTAGAGCTGGTAGACTTTAATCTA 1630
Qy 2238 AAAGTCCCTTT---GTTTGAAGACAGCCCTCCCTGCTGCCCAAGATTTTCATTTCAATGCCA 2294
Db 1631 ATGCCAACTTACCCTCGGAAACGTCGAGGAATCTGCGCAAGTCTTTCACCTCTTCTCGG 1690
Qy 2295 CGTTTTGTAAAGTTTCTTCAGATGAGGAAAGGAGTGTCTGCTCCATGACCAAGATTTCTC 2354
Db 1691 CGTTTCGTCGCGACCTCCAGATAATGGAAGAGGAGTTTGTGGCCATGGTCAGGATCTC 1750
Qy 2355 CTGTACTTGTAAAGGTGCGACAAAGCCCTGGTGTGCTGAGGAGGAGATTTGCCAATATGCTT 2414
Db 1751 CGTACTTGTGGATAATTTCTGCACAGCTTGTGGAAACGCGACCACTACTGATCTTAAC 1810
Qy 2415 CAGTGGGAGGAGCTGGAGTGGCAGAAATATGACAGAAATATGCAAGGCAATGATTTGTACC 2474
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Db	1811	CAGATTAGTCAGAGCGAGTGGCAAACTACGTGGACTTATAAGGGAAATGCTGGTCACC	1870
Qy	2475	AACCTGGGACGAAACCAAGCTCTGTCCGATCGATCAATCGGATCGTGAAACAGTTCAA-	2533
Db	1871	AAGCGGGTTATAAGCGCTGTTCCGTACCGTGTGACCAATTTGGACAGGAATAATCCCGAT	1930
Qy	2534	-----CCCCGATGTGATTAATTTTCCGATTAATCGTCACATTTGGG	2573
Db	1931	TTGCCCGAGTCGTAGATCGGAGACTGGAATCTCACATCCAGCAATCTGTCACATTTGGC	1990
Qy	2574	ATACGCCCTGCAAGTTATGAGTTATGAGAGACCCACAGTACCAAAACCTGTGGAGAGT	2633
Db	1991	ATTGTCATCTCTCAGCTAAGCTACGCTCGGAATCCAGAGTACCAAGCGGTGGCGAGAG	2050
Qy	2634	TATGTGAACCTTCGCCACTCTCTAGCAATAGTCCAAAGTCAAACTGACAAAACAG	2693
Db	2051	TACGTTAAGTACCGTCATCTGATGGCAACATGTGAGAGCCCTCTTTCAAGGATAAGGCG	2110
Qy	2694	AGCTGGCACAGAGGAGGAAGCCCTCCAAAATAACGCAAGAAATCAATGAGACGA	2753
Db	2111	AAGCTAGAGGAGAGGACGAACGTCTTCAGGAGATCGGAACCTCAGGGGCGCATGAAACGA	2170
Qy	2754	GAAGTAAACGGTGGAGCTAAGTAGACCAAGATTCTGGAAACTGGGCATCGTTCTGATGTC	2813
Db	2171	AATATCACAGTGGCGATCAGCTCGAGGGCTTCTATCGCACCGGCATTAATGCGGACGTT	2230
Qy	2814	TGTCAGCATGCAATGATGTACTGTTCTGACCCATCATATCCGTACCAACCAATGCCTA	2873
Db	2231	GTGACAGTGCCTATGTTGATCTCTGCTTAACTTGGTCACTTCGCTTCAACGTCGCTG	2290
Qy	2874	ATGCAATTTGGACAAGTTGATAGGATATATCTTCCAAGATCGTTGTCTGTTGACGTGGCC	2933
Db	2291	GACCTGCTAGAGAGATATCGGGTACCGCTTTAAAAATCGGTACCTTCTCCAATTTGGCG	2350
Qy	2934	ATGACTCATCAAGTCATCAATTAATTTTGGAAATGATCTCATGATCCAGCAATTTCA	2993
Db	2351	CTGACGCATCCCTCATCAAGGAGAACTACGGTACCAATCCGATACGCGCGGTAAATCG	2410
Qy	2994	TTATCTAATCTGTGGAAATTCGGGAGCCCAATACGGACAGAAAGTTTCATCATGACAC	3053
Db	2411	CTGACTAATCTCGGAATTCGTACGCGAGTACGGAGATCGCAAGATCCATTAATCAAC	2470
Qy	3054	ATCGGGAAGAAAGGATTAACACCTTGTATTAATATCATGTACGCTTGGCCAGATGAC	3113
Db	2471	ACAGCGAAGGGGTATCAACACATTAAGTGTAGCATTTATGTCCAGATTTGGCAAGGACAT	2530
Qy	3114	CCAACTCCCTCGAGGATTAACCAATGAACGGTTGGAAATTCCTGGGTGATGCTGTTGTT	3173
Db	2531	GAGACTGTTTCGAACATAACCCCAATGAGAGACTAGAGTTCTCGGGTGTGCTGTAGTA	2590
Qy	3174	GAAATTTTCAGCAGCGTCCATTTGTACTATTTGTTTCTAGTCTGGAAAGAGGAGGATTA	3233
Db	2591	GAAATTCCTCAGCTCAATCAATCTGTTTATGTTCCCTGAACTGGAGAGGGTGTGTTG	2650
Qy	3234	GCAACTATCGAGCTGCATTTGTCAGAAATCAGCACCTTGGCCATAGCAAGAAACTT	3293
Db	2651	GCCACTTACCGAGCGCAATTTGTCGAACACAGCACTTGGCTCTGTTGGCCAAAAGCTG	2710
Qy	3294	GAACTGGATPCCATTTATGCTGATGCTACAGGCGCTGACCTTTGTAGAGAACTCGACCTT	3353
Db	2711	CAACTGGAGAGTTTATGCTGTACGCAACGATCCGATCTGTGCCACGAGTTGGAATG	2770
Qy	3354	CGACATGCAATGCCAATTTTTCAGAGGTTAATAGGAGCTGTTTACTTGGAGGGAAGC	3413
Db	2771	CGTACGCCATGCCAACTGTTTGAAGCCCTAATGGCGCGCTTCTATTTGGATGTTGA	2830
Qy	3414	CTGGAGGAAGCCAGCAGTTATTTGGACGCTTCTCTTTA---ATGATCCGACCTGGCG	3470
Db	2831	ATCAAGGTGGCAGATGAGGTGTTTACGGATGCACTCTTCGGGACGAGCAACCTGCTG	2890
Qy	3471	GAACTGCGCTCAATTTATCTCTCCACCCACTCAACTACAGAGCCAAATCTGATCGA	3530
Db	2891	AGTATATGGAAGAAATCTGCCGAGCACCCCGTTGCGAGAACAGGAGCCACTTTGGGATCGC	2950
Qy	3531	CAACTTATTTGAAACTTCTCCAGTTCTACAAAACCTTACTAGTTTGAAGAGCAATTTGGA	3590
Db	2951	AGCTGTATTTGATTTCTTACCGGTGCTTTAAGGAGTTAAACCAATTTGAGGACTCTTATTGGA	3010
Qy	3591	GTAATTTTACTCATGTTTCGACTTCTGGCAAGGCACTTCAATTTGAGAACTTGTGGGATTT	3650
Db	3011	ATCAAGTTTAAAGCAATTTGGCTTTTGGCTCGCGCTTTTACCGATCGCTCCATTTGGTTTC	3070
Qy	3651	AACCATCTGACCTTAGGCCACAATCAGAGAAATGGAATTCCTAGTGTACTCCATAATATGCA	3710
Db	3071	ACCCACTTGACCTTTGGGTCAATCAGCGTTTAGAGTTCTTTGGGCGACACAGTGTGTCAG	3130
Qy	3711	CTGGTAGCCACACAGAGTACTTATTCATTTCCAGATCATCATGAAGGACACTTAAT	3770
Db	3131	CTGATTTGCTCGGAGTACTTATCGTCACTTCCCTGAGCACCCAGAGGGCCACTTTGTCC	3190
Qy	3771	TTGTTGCGAAGCTCTTTGGTGAATCAATTTATTTGAGCGCTGTACACTGATTAAGGATTTGGAA	3830
Db	3191	CTGCTACGATCTCTCAATGATCGCACTCAAGCGGTGTTTTCGATGATTTGGGA	3250
Qy	3831	ATGCAAGGATCGCCATAACCAACGACAAAGAGAGGCTGTGGCGCTTCGACCAAG	3890
Db	3251	ATGCCGAAATATGC-----CGTGTATGCCAATCCCAAGGCTGATTTGAAGACCAAA	3301
Qy	3891	ACCTTGGCGGAGCTTTTGGAAATCAATTTATTTGAGCGCTGTACACTGATTAAGGATTTGGAA	3950
Db	3302	GATCGTCCGATCTGCTGGAGGCAATTCCTCGGCGCTCTGTACGTGACAAAGGCTCTCTTG	3361
Qy	3951	TATGTTCAATCTTCAATGATGCTCTTCTTCCACAGATTTGAAGAAATTCATTTTGAAT	4010
Db	3362	TATTTGAAACAGTTTGGCCATGTATGTTTGTTCCTCCCGACTTCAGTTGTTTATCAATGAT	3421
Qy	4011	CAGGATTTGAAATGACCCCAATCCAGCTTCCAGCTTTCAGCTGTTTGTGACACTTAGACA---	4067
Db	3422	CAGGACTGGAAACGATCCCAAGTCAAGCTGCAAGCTGCAAGTGTGCTCCTCACACTTCGCACAATG	3481
Qy	4068	GAAGGAAAAGAGCGACGACATTCCTCTGTGTACAAAGCTCTGACAGACAGTGGGCCCCATCCCAT	4127
Db	3482	GATGGCGGCGAGCGGACATTCCTACTACAAGTGTGTGGAGGCCAGTGTGTCCAACTAAT	3541
Qy	4128	GCCGGAACCTTACACTGTGGCTGTTTATTTCAAGGGAGAAAGATAGCTGTGGGAAAAGGA	4187
Db	3542	ACGCGGTATACAGGTGGCGCTTTATTTCCGCTCAAGCGGCTGGCCACTTCAAGTGGC	3601
Qy	4188	CCAAGTATTCAGCAAGCGGAAATGGGAGCAGCAATGATGCTGCTTGAATAAT-----AT	4241
Db	3602	TCCTTCCATTCAGCAGGCGGAGATGAACGCCGCTAAGCAGCGCTGGAGAAATTCAGGGAC	3661
Qy	4242	AATTTTCCCAAGATGGCCCATCAGAAAGCGGTTTCATCG	4278
Db	3662	CTGTTTCCCACTGGATCACCAAAAGCGCGTGTATCG	3698
RESULT 13			
US-11-097-143-2407/c			
; Sequence 2407, Application US/11097143			
; Publication No. US20050208558A1			
; GENERAL INFORMATION:			
; APPLICANT: Venter, J. Craig			
; APPLICANT: et al.			
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID			
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE			
; FILE REFERENCE: DROSOPHILA GENES.			
; CURRENT APPLICATION NUMBER: US/11/097,143			
; PRIOR FILING DATE: 2005-04-04			
; PRIOR APPLICATION NUMBER: 60/157,832			
; PRIOR FILING DATE: 1999-10-05			
; PRIOR APPLICATION NUMBER: 60/160,191			
; PRIOR FILING DATE: 1999-10-19			
; PRIOR APPLICATION NUMBER: 60/161,932			

;
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2407
; LENGTH: 6397
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-2407

Query Match 14.8%; Score 703.8; DB 10; Length 6397;

Best Local Similarity 57.0%; Pred. No. 2.9e-189;
Matches 1490; Conservative 0; Mismatches 1022; Indels 103; Gaps 7;

Qy	1758	ATTGCGAATCAAAACGCAAAAGGCCACCTGACCGACTTCATGATGAATTTGGTAC	1817
Db	4247	ATGGAGAGCTTTCGCGCAAGGTGCAACATCCGACGGTGTGCACGCGATCTCTGGCAC	4188
Qy	1818	AACGATCCAGCGCAGATGAATGATGGACCACTCTGCAAAATGCGAGCGCAAGCAAGCGC	1877
Db	4187	AACGACGCGGTGAGATGAACGACGAGACCTCTTTGCGCGTCTCAGCCAAAGTCCCGGCGC	4128
Qy	1878	ACAGGAATAGGCACAGCATTTATCTGGAGAGAGGCCATCAAGCCCTGTCTGCTATG	1937
Db	4127	ATTGGCATTCGACGCGCATATATCCGGGCGAGCTGGCTTATAAGTTGTGCGATCCAAAC	4068
Qy	1938	ACCAACAATCTGCGACATTTTCCACTACCGATCACGCTCTCCCGCCTACGAACTTT	1997
Db	4067	AGCAACATGCGAGCAGCTGTTCCTACATCAGGATCAGATCTACCGCCCATTAATTC	4008
Qy	1998	TTAACTGACAGGCGCACTGTTATAGAAATACGATGATCAGCAGTATATCTTTGAAGGATTT	2057
Db	4007	CTGCAAAAGACACCCACCATTAACGATGATGAGCAGGTTTCTATTTCGAGGCTTC	3948
Qy	2058	TCATGTTTGCACATGCCCCCTGACCAATATTCCACTGTGTAAGTAATTAATTAATCAAC	2117
Db	3947	TCATTTCTCTCGCATGTGCTCTCCGATCTGCGCTCTGCAAGGTGATCCGCTTCAAC	3888
Qy	2118	ATAGACTACAGATTCATTTTCAATGAGAGATGATGCGGAGAAATTTTGTGTGAAGGG	2177
Db	3887	ATCGAGTACACCATTTGATGACGAGAGAGAGATGCCAGAACTTACCATCCACGAG	3828
Qy	2178	CTTGAACTCTTTTCACTGTTT-----	2197
Db	3827	CTAGACATTTTGTGAAGTAAATTTGAGATTTTCTTTATAGCAATTAATTAATCTTAT	3768
Qy	2198	-----CTATTTCAGAGATATTTTGGAAATTAATGACTGGAAATCTTAA	2239
Db	3767	CTCAATTTTCAGTCAAAATACCTGTTTCATGAACCTGTAGAGCTGGTGAATTAATCTAAT	3708
Qy	2240	AGGTCCTTTT---CTTTGACAGACGCTCCCTGCTGCGCAAGATTTTCAATTTCAATGCCAG	2296
Db	3707	GCCCAACTTACCCTCCGGAACCTGAGGAATCTCTGCCAGCTTTTCACTTTCTTCGCG	3648
Qy	2297	TTTGTGAAGATTTCTTCCAGATGGAGAAAGGAGTGTCTCCATGACCAAGATTTCTCT	2356
Db	3647	TTTGTGCGGACCTGCCAGATTAATGGAAGAGAGTTTGGCCATGCTCGAGGTACTCCG	3588
Qy	2357	GTACTTTTAAAGTGCAGCAAGCCCTGTGCTGCTGAGGAGAGATTTGCCAATATGCTTCA	2416
Db	3587	CTACTTGTGGAATAATTCGACAGCTTTGTGGAACGCGCAGCAACTACTGTCATCTTAAACA	3528
Qy	2417	GTGGGAGGAGCTGGAGTGGCAGAAATATGCAAGAAATGCAAGAGGATGATTTGTTACCA	2476

Db	3527	GATTAGTCAGAGCGAGTGGCAAAACTACGTGGAGCTTCATAAAGGAATGCTGGTCCACAA	3468
Qy	2477	CCCTGGGACGAAACCAAGCTCTGTCCGTATCGATCAACTGATCGTGAAACAGTTCAA---	2533
Db	3467	GCGGGTTATAAGCCGTGTTCGCTACCGTTTGAACAATTCGACAGGAATAACTCCGATTT	3408
Qy	2534	-----CCCCGATGTGATTAATTTTCCGATTAATCGTCCACTTTGGGAT	2575
Db	3407	GCCGAGTGTGATGTCGAGACTTGGAAATCTCATCCAGCAATCGTGCACATTTGGGAT	3348
Qy	2576	ACGCCCTGACAGTTGAGTTATGACGAGAGACCCACAGTACCAAAACCTGTGGAAAGAGTTA	2635
Db	3347	TTGTCACTCTCAGTAACTACGCTGGAATCCAGAGTACCAAGAGGCGTGGCGAGGTA	3288
Qy	2636	TGTGAAACTTTCGCCACCTCTAGCAATAGTCCCAAGTCAAAACAACTGACAAACAGAA	2695
Db	3287	CGTTAAGTACCGTCACTGATGCGCAACATGTGGAAGCCCTCTTTCAAGGATAAGCGCAA	3228
Qy	2696	GCTGGCACAGAGGAGGAGGCCCTCCAAAATAACGCGAGAGAAATACAATGAGACGAGA	2755
Db	3227	GCTAGAGGAGAGAGGACACGCTCTTCAGGAGATGCGAACTCAGGGGCGCATGAACGAA	3168
Qy	2756	AGTAAACGCTGAGCTAAGTAGCCAAAGATTTCTGGAAAACCTGGCATCCGTTCTGATGCTG	2815
Db	3167	TATCAGTGGCGATCAGCTCGGAGGCTTCTATCGCACCGCATTAATGTGCGACGTTGT	3108
Qy	2816	TCAGCATGAATGATGCTACTGTTCTGACCCATCATATCCGCTACCAACATGCCTAAT	2875
Db	3107	GCAGCATGCCATTTGATTTCTGCTCTTAACCTGCTGCTTCTGCTTTTCAAGTCCGCTGA	3048
Qy	2876	GCATTTGGCAAGTTGATAGGATATACTTTTCCAAAGATCGTTGCTGTGAGCTGGCCAT	2935
Db	3047	CCTGCTAGAGGAGAGTATCGGGTACCGCTTTTAAATAATTCGGTACCTTCTCCAAATGGCGCT	2988
Qy	2936	GACTCATCCAAAGTCATCAATTTAAATTTTGGAAATGAAATCTCTGATCATGCCAGGAATTCAT	2995
Db	2987	GAGCATCTCTCATACAGGAGAACTACGCTACCAATCCGGATCAGCCCGCTAATTCGCT	2928
Qy	2996	ATCTAACTGTGGAATTCGGCAGCCCAAAATACGAGACAGAAAGTTTCAATCAATGACAT	3055
Db	2927	GACTAACTGCGGAATTCGTGAGCGGAGTACGAGAGTCCGCAAGATCCATTAATACATGAAC	2868
Qy	3056	GCGGAGAAAGGATTAACACCTTTGATAATATCATGTACGCTTGGCCCAAGATGACCC	3115
Db	2867	ACCAAGCGGGTATCAACACATTTAGTAGCATTTATGTCCAGATTTTGGCAAGGAGCATGA	2808
Qy	3116	AACTCCTCGAGATTAACCAACATGAACGTTTGGAAATTCCTGGGTGATGCTGTGTTGA	3175
Db	2807	GACTGTTTGGACATTAACCAACATGAAGACTAGAGTTCTCGGTGATGCTGTAGTAGA	2748
Qy	3176	ATTTCTGACCGCGTCCATTTGATTAATTTTCTTCTGAGTGTGGAAGAGGAGATTAGC	3235
Db	2747	ATTCCTCAGCTCAATCCATCTGTTTATGTTTCCCTGAACTGAGAGGGTGGTTTGGC	2688
Qy	3236	AACCTATCGGACTGCTGTTTTCAGAAATCAGACACTTGGCATGCTAGCAAGAACTTGA	3295
Db	2687	CACCTTACCGAGCGCAATTTGTCCAAAACCCAGCACTTGGCTCTGTGGCCAAAAGCTGCA	2628
Qy	3296	ACTGGATCCATTTATGCTGATGCTCAACGCGCTGACCTTTGTAGAGAACTCGGACCTTCG	3355
Db	2627	ACTGGAAGAGTTTATGCTGTACGCAACCGATCCGATCTGTGCGCAGATTTGNACTGCG	2568
Qy	3356	ACATGCAATGGCCAAATTTTGAAGCTTAAATAGGAGCTGTTTACTTGA---GGGAAG	3412
Db	2567	TCAGCCATGGCCAACTGTTTGAAGCCCTTAATGGGCGCGCTTCTATTGATGGTGAAT	2508
Qy	3413	CTTGGAGGAGCCACAGCTTATTTGACGCTTCTTTTAATGATCCGACCTTCGCGCA	3472
Db	2507	CRAAGTGGCAGATGAGGTGTTACGATGCACTCTTCCGCGAGGACGAGAAATGCTGAG	2448
Qy	3473	AGTCTGCTCAATTTATCTCTCCACCCACTCCAACTACAGAGCCAAATACTGATCGACA	3532
Db	2447	TATATGAAAGAAATCTCGCGAGCACCCGTTGCAAGAACAGAGCCACTTGGGATCCAG	2388

Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20941
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 598, 632, 633
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20941

Query Match 9.9%; Score 469.4; DB 8; Length 633;
Best Local Similarity 98.5%; Pred. No. 8.1e-123;
Matches 473; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 58 GAGAGCCTTTTATAGGTTGCTTTCCCGGGGATGTGAAGGATACAGAAATGACTGTGAAT 117
DB 152 GAGTTACTTTTCAGGTTGCTTTTCGGGGATGTGAAGGATACAGAAATGACTGTGAAT 211
QY 118 CAACCCATATCATCAGGAGCTGATATCTAGTGGAGAGTTAGACGTGTGCATCTTCA 177
DB 212 CAACCCATATCATCAGGAGCTGATATCTAGTGGAGAGTTAGACGTGTGCATCTTCA 271
QY 178 CTATGATATGAGGAGCTCTCTGAGCTTATATCTCTGTGGAAGATGTGACATATCCAGGC 237
DB 272 CTATGATATGAGGAGCTCTCTGAGCTTATATCTCTGTGGAAGATGTGACATATCCAGGC 331
QY 238 GGAACATCATGTCAGGGAACACATGTCCAGAGATGTCTCCACCCGGGAGGAGGC 297
DB 332 GGAACATCATGTCAGGGAACACATGTCCAGAGATGTCTCCACCCGGGAGGAGGT 391
QY 298 GTCCCGAGGACGAGGAGACATGGAGCCAGACCTCAGCACCATCTCTTAGGCCCCCAA 357
DB 392 GTCCCGAGGACGAGGAGACATGGAGCCAGACCTCAGCACCATCTCTTAGGCCCCCAA 451
QY 358 ATCTGAGGCTGCTTCAACCTCAGAGCCTCTGTGCAATATCAATATGAACCTCCAAGTG 417
DB 452 ATCTGAGGCTGCTTCAACCTCAGAGCCTCTGTGCAATATCAATATGAACCTCCAAGTG 511
QY 418 CCCCTTCCACCACTTTCTCAACTCTCCAGCCCAATTTCTCCCTCCAGCAGCACT 477
DB 512 CCCCTTCCACCACTTTCTCAACTCTCCAGCCCAATTTCTCCCTCCAGCAGCACT 571
QY 478 TTGTACCCCTTCCCAACCACTCTCCGTCAGGCAAGGCCCTCTTCCCTCCGCCCCAA 537
DB 572 TTGTACCCCTTCCCAACCACTCTCCGTCAGGCAAGGCCCTCTTCCCTCCGCCCCAA 631

Search completed: December 27, 2005, 04:23:16
Job time : 3516 secs

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Qy	61	AGCCTTTTATAGTTCCTTTCCGGGGATGGAAGATACAGAAATGATGTGAATCAA	120
Db			
Qy	61	AGCCTTTTATAGTTCCTTTCCGGGGATGTGAAGATACAGAAATGATGTGAATCAA	120
Db			
Qy	121	CCCATATCATCAAGGAGCTGATTAATCTAGTGGAGAGTTAGAGTGTGCATACTTCACTA	180
Db			
Qy	121	CCCATATCATCAAGGAGCTGATTAATCTAGTGGAGAGTTAGAGTGTGCATACTTCACTA	180
Db			
Qy	181	TGATATGAGGAGCTCTGAGCTTATATCTCTGTGGAAGATGTGCATATCCAGCGGA	240
Db			
Qy	181	TGATATGAGGAGCTCTGAGCTTATATCTCTGTGGAAGATGTGCATATCCAGCGGA	240
Db			
Qy	241	ACATCATGATGCAAGGAAAACATGTGCACAGAAATGCTTTCCACCCGGGACGAGGGCTC	300
Db			
Qy	241	ACATCATGATGCAAGGAAAACATGTGCACAGAAATGCTTTCCACCCGGGACGAGGGTGC	300
Db			
Qy	301	CCCGAGGACGAGGAGCATGGAAGCCAGCCCTCAGGACCATCTTTAGGCCCCAAATC	360
Db			
Qy	301	CCCGAGGACGAGGAGCATGGAAGCCAGCAGCCCTCAGCACCATCTTTAGGCCCCAAATC	360
Db			
Qy	361	TGAGGCTGCTTACCCCTCAGCAGCCCTCTGTGCAATATCAATATGAACCTTCCAAAGTGCCC	420
Db			
Qy	361	TGAGGCTGCTTACCCCTCAGCAGCCCTCTGTGCAATATCAATATGAACCTTCCAAAGTGCCC	420
Db			
Qy	421	CTTCCACCACTTCTCAAACTCTCCAGCCCCCAATTTCTCCCTCCACGACGAGCTTTG	480
Db			
Qy	421	CTTCCACCACTTCTCAAACTCTCCAGCCCCCAATTTCTCCCTCCACGACGAGCTTTG	480
Db			
Qy	481	TACCTTTCCCCCAACCATGCTCCGTCAGGCGAAGGCCCTTTCCGCCCTGCGCCATCA	540
Db			
Qy	481	TACCTTTCCCCCAACCATGCTCCGTCAGGCGAAGGCCCTTTCCGCCCTGCGCCATCA	540
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Qy	541	GGCGCCCTTTCCCAACCAACAGATGAGGACCCCTTCCAGTTCTCTTGTGTTTCTC	600
Db			
Qy	541	GGCGCCCTTTCCCAACCAACAGATGAGGACCCCTTCCAGTTCTCTTGTGTTTCTC	600
Db			
Qy	601	CCATGCCACCAACCAATGCTTGTCTTAATAACCCCCAGTCCCTGGGGGACCTCTCGAC	660
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Qy	601	CCATGCCACCAACCAATGCTTGTCTTAATAACCCCCAGTCCCTGGGGGACCTCTCGAC	660
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Qy	661	AAGGCACTTTCCCTTATGATGCCCCCTCTCCATGCTCATCCCGGCCCTCCAG	720
Db			
Qy	661	AAGGCACTTTCCCTTATGATGCCCCCTCTCCATGCTCATCCCGGCCCTCCAG	720
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Qy	721	TCATGCCGACGAGTTAAATTAATCAGTACCTCCGGGCTATTCTCACCAACTTCCAC	780
Db			
Qy	721	TCATGCCGACGAGTTAAATTAATCAGTACCTCCGGGCTATTCTCACCAACTTCCAC	780
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Qy	781	CTCCAGTTTAAATAGTTTCCAGAACCAACCTAGTTCCTTCTGCCCCAGTGTCTAATAACA	840
Db			
Qy	781	CTCCAGTTTAAATAGTTTCCAGAACCAACCTAGTTCCTTCTGCCCCAGTGTCTAATAACA	840
Db			
Qy	841	GCAGTAGTCTCATTTTCAGACATCTCCCTCCATACCCACTCCCAAGGCTCCAGTGAGA	900
Db			
Qy	841	GCAGTAGTCTCATTTTCAGACATCTCCCTCCATACCCACTCCCAAGGCTCCAGTGAGA	900
Db			
Qy	901	GAAAGTCCCCAGAAAGGCTGAAAACATATGATGACCAAGGACCGAGACCAAGTCAATG	960
Db			
Qy	901	GAAAGTCCCCAGAAAGGCTGAAAACATATGATGACCAAGGACCGAGACCAAGTCAATG	960
Db			
Qy	961	GGCGAGGTGAGGAGCATCGCTCCCTGGATCGCGGGAGCGAGGCCGAGTCCCGACAGGA	1020
Db			
Qy	961	GGCGAGGTGAGGAGCATCGTCCCTGGATCGCGGGAGCGAGGCCGAGTCCCGACAGGA	1020
Db			
Qy	1021	GAAACAAGACAGCCGGTACAGATCTGATTATGACCCGAGGAGAACACATCTCGCCACC	1080
Db			
Qy	1021	GAAACAAGACAGCCGGTACAGATCTGATTATGACCCGAGGAGAACACATCTCGCCACC	1080
Db			
Qy	1081	GCAGTACGAAACGAGACGAGCAGAACCGGAGAGACACAGGCGATCGAGACACCGAA	1140
Db			
Qy	1081	GCAGTACGAAACGAGACGAGCAGAACCGGAGAGACACAGGCGATCGAGACACCGAA	1140
Db			
Qy	1141	GATCACCCTCTCTGGAAGGTCCTTCAAAAAAGAGTATAAGAGATCTGGAAGGAGTTACG	1200
Db			
Qy	1141	GATCACCCTCTCTGGAAGGTCCTTCAAAAAAGAGTATAAGAGATCTGGAAGGAGTTACG	1200
Db			
Qy	1201	GTTTATCGGTGTTCTCTGAACTCTGTCGATGCACACAGAAATTAACCTGGGGAGATTATTA	1260
Db			
Qy	1201	GTTTATCGGTGTTCTCTGAACTCTGTCGATGCACACAGAAATTAACCTGGGGAGATTATTA	1260
Db			
Qy	1261	AAAAATACAGATCTTTGGGGCCCCCCTCGGAGATGTGTAATCATCGCTCCCAAGTAGGG	1320
Db			
Qy	1261	AAAAATACAGATCTTTGGGGCCCCCCTCGGAGATGTGTAATCATCGCTCCCAAGTAGGG	1320
Db			
Qy	1321	AGAAGAAGAGAGCTCGTTGGGAGGAGAAAAAGACCGTTGGAGTGCAACACAGAGTTCTG	1380
Db			
Qy	1321	AGAAGAAGAGAGCTCGTTGGGAGGAGAAAAAGACCGTTGGAGTGCAACACAGAGTTCTG	1380
Db			
Qy	1381	GCAAGACACAGAACTATATCTCAATCAAGGAAAAAGAGCCCGAGGAGACCATGCTGTACA	1440
Db			
Qy	1381	GCAAGACACAGAACTATATCTCAATCAAGGAAAAAGAGCCCGAGGAGACCATGCTGTACA	1440
Db			
Qy	1441	AGATGAGGAGGAGAAAGAACTTTCTTAAGCCTGTGTGGATTCGATGCACCTCATTTAG	1500
Db			
Qy	1441	AGATGAGGAGGAGAAAGAACTTTCTTAAGCCTGTGTGGATTCGATGCACCTCATTTAG	1500
Db			
Qy	1501	AAAACTACTCTCCAGTACCCCATGATCAGGTGGGAGATTTCTACAGTGGTTGGAACGA	1560
Db			
Qy	1501	AAAACTACTCTCCAGTACCCCATGATCAGGTGGGAGATTTCTACAGTGGTTGGAACGA	1560
Db			
Qy	1561	GTAGGCTTCTGTGATTTATGACAAATTTGAGGAGAGTTGGGGAGCAGGCAAGAAAGG	1620
Db			
Qy	1561	GTAGGCTTCTGTGATTTATGACAAATTTGAGGAGAGTTGGGGAGCAGGCAAGAAAGG	1620
Db			
Qy	1621	CCAAAGTGTCTGGCTCCGTGGGAACCTTCAAGAGGAGCTCGATGAAGATTTAGAGA	1680
Db			
Qy	1621	CCAAAGTGTCTGGCTCCGTGGGAACCTTCAAGAGGAGCTCGATGAAGATTTAGAGA	1680
Db			
Qy	1681	GTTCAGTGAATCCGAGTGTGAGTCTGTAGGACACAGCACTGTCTTAGCAGCTCAGACT	1740
Db			
Qy	1681	GTTCAGTGAATCCGAGTGTGAGTCTGTAGGACACAGCACTGTCTTAGCAGCTCAGACT	1740
Db			
Qy	1741	CTGAAAGTTTGTGAGCTTTATTTGACAGAAATCAAAACGAAAAAGGCCACCTTGACCGACTTC	1800
Db			
Qy	1741	CTGAAAGTTTGTGAGCTTTATTTGACAGAAATCAAAACGAAAAAGGCCACCTTGACCGACTTC	1800
Db			
Qy	1801	ATGATGAATCTTTGGTCAACAGATCCAGGCCAGATGAATGATGACCACTCTGCAAAATGCA	1860
Db			
Qy	1801	ATGATGAATCTTTGGTCAACAGATCCAGGCCAGATGAATGATGACCACTCTGCAAAATGCA	1860
Db			
Qy	1861	GGCAGAAAGGCAAGACGACACAGGAATTAGGCACAGCACTTTATCTTGGAGAGAGGCCATCA	1920
Db			
Qy	1861	GGCAGAAAGGCAAGACGACACAGGAATTAGGCACAGCACTTTATCTTGGAGAGAGGCCATCA	1920
Db			
Qy	1921	AGCCCTGTCTCTATGACCAACAAATGCTGGCAGACTTTTCCACTACCGGATCAAGTCT	1980
Db			
Qy	1921	AGCCCTGTCTCTATGACCAACAAATGCTGGCAGACTTTTCCACTACCGGATCAAGTCT	1980
Db			
Qy	1981	CCCCCGCTACGAACTTTTAACTGACAGGCCAACTGTTATAGATACGATCATCCAGGT	2040
Db			
Qy	1981	CCCCCGCTACGAACTTTTAACTGACAGGCCAACTGTTATAGATACGATCATCCAGGT	2040
Db			
Qy	2041	ATATCTTTGAGGAGTTTCTATGTTTGCATGTCACATGCCCTGACCAATATTTCCATGTGTA	2100
Db			
Qy	2041	ATATCTTTGAGGAGTTTCTATGTTTGCATGTCACATGCCCTGACCAATATTTCCATGTGTA	2100
Db			
Qy	2101	AAGTAATTAGATTCAAACATAGACTACAGATTCATTTCAATTGAAGAGATGATGCCGAGA	2160
Db			
Qy	2101	AAGTAATTAGATTCAAACATAGACTACAGATTCATTTCAATTGAAGAGATGATGCCGAGA	2160
Db			
Qy	2161	ATTTTGTGTGAAAGGGCTTGAACTCTTTTACCTGTTCTTATTCAGAGATATTTTGGAAAT	2220
Db			
Qy	2161	ATTTTGTGTGAAAGGGCTTGAACTCTTTTACCTGTTCTTATTCAGAGATATTTTGGAAAT	2220
Db			
Qy	2221	TATATGACTGGAACTTTAAAGGTCCTTTGTTTGAAGACAGGCCCTCCCTGCTGCCCAAGAT	2280
Db			

|||||
2221 TATATGACTGGAACTTAAAGTCTTTTGTGTTGAAGACAGCGCTCCCTGCTGCCCAAGAT 2280
QY
2281 TTCAATTCATGCCACGTTTTGTAAGATTTCTTCCAGATGGAGGAAGAAAGTGTGTCCA 2340
Db
2281 TTCAATTCATGCCACGTTTTGTAAGATTTCTTCCAGATGGAGGAAGAAAGTGTGTCCA 2340
QY
2341 TGCACCAAGATTTCTCTGTACTTTGTTAAGTGTGACGCAAGCCCTGGTCTCAGGAGGAGA 2400
Db
2341 TGCACCAAGATTTCTCTGTACTTTGTTAAGTGTGACGCAAGCCCTGGTCTCAGGAGGAGA 2400
QY
2401 TTGCCAATATGCTTCAGTGGAGGAGCTGGAGTGGCAGAAAATATGCAAGAAATGCAAAAG 2460
Db
2401 TTGCCAATATGCTTCAGTGGAGGAGCTGGAGTGGCAGAAAATATGCAAGAAATGCAAAAG 2460
QY
2461 GCATGATTTGTTACCAACCTCGGACGAAACCAAGCTCTGTCCGTATCGATCAACTGGATC 2520
Db
2461 GCATGATTTGTTACCAACCTCGGACGAAACCAAGCTCTGTCCGTATCGATCAACTGGATC 2520
QY
2521 GTGAACAGTTCAACCCCGATGTGATTAATTTTCCGATTAATCGTCCACTTTGGGATACGCC 2580
Db
2521 GTGAACAGTTCAACCCCGATGTGATTAATTTTCCGATTAATCGTCCACTTTGGGATACGCC 2580
QY
2581 CTGCACAGTTGAGTTATGTCAGAGACCCACAGTACCAAAAACCTGTGGAAGAGTTATGTGA 2640
Db
2581 CTGCACAGTTGAGTTATGTCAGAGACCCACAGTACCAAAAACCTGTGGAAGAGTTATGTGA 2640
QY
2641 AACTTCCGCCACTCTAGCAAAATAGTCCAAAGTCAAAACCTGACAAAACAGAAAGCTGG 2700
Db
2641 AACTTCCGCCACTCTAGCAAAATAGTCCAAAGTCAAAACCTGACAAAACAGAAAGCTGG 2700
QY
2701 CACAGAGGGAGGAGCCCTCCAAAATATACGGCAGAGAGATACATGAGACGAGAGTAA 2760
Db
2701 CACAGAGGGAGGAGCCCTCCAAAATATACGGCAGAGAGATACATGAGACGAGAGTAA 2760
QY
2761 CGGTGGAGCTAAGTAGCAAGGATTTCTGGAATACTGGCATCCGTTCTGATGCTGTGACG 2820
Db
2761 CGGTGGAGCTAAGTAGCAAGGATTTCTGGAATACTGGCATCCGTTCTGATGCTGTGACG 2820
QY
2821 ATGCAATGATGCTACCTGTTCTGACCCCATCATATCCGCTACCAACCAATGCCATATGCATT 2880
Db
2881 TGGCAAGTTGATAGGATATACCTTCCAAAGATCGTTGTCTGTGACGCTGCCATGACTC 2940
Db
2881 TGGCAAGTTGATAGGATATACCTTCCAAAGATCGTTGTCTGTGACGCTGCCATGACTC 2940
QY
2941 ATCCAGTGCATCATTTAAATTTTGGAAATGAAATCTGATCATGATCCAGGAATTCATTATCTA 3000
Db
2941 ATCCAGTGCATCATTTAAATTTTGGAAATGAAATCTGATCATGATCCAGGAATTCATTATCTA 3000
QY
3001 ACTGTGGAATTTGGCAGCCCAAAATACGGAGACAGAAAAGTTTCATCATGTCACATGCGGA 3060
Db
3001 ACTGTGGAATTTGGCAGCCCAAAATACGGAGACAGAAAAGTTTCATCATGTCACATGCGGA 3060
QY
3061 AGAAAGGATTAACACTTGTGATAATATCATGTGATGTCACGCTTGGCCAAAGATGCCAACTC 3120
Db
3061 AGAAAGGATTAACACTTGTGATAATATCATGTGATGTCACGCTTGGCCAAAGATGCCAACTC 3120
QY
3121 CCTCGAGGATTAACCAATGAAACGTTGGAATTTCTGGGTGATGCTGTTGTTGAAATTC 3180
Db
3121 CCTCGAGGATTAACCAATGAAACGTTGGAATTTCTGGGTGATGCTGTTGTTGAAATTC 3180
QY
3181 TGACCAAGCTTCAATTTGTAATTTGTTTCTAGTCTGGAGAGGAGGATTAAGCACTT 3240
Db
3181 TGACCAAGCTTCAATTTGTAATTTGTTTCTAGTCTGGAGAGGAGGATTAAGCACTT 3240
QY
3241 ATCGGATGCAATTTGTTGATAATCAGCACTTGGCCATGCTAGCAAGAAACCTTGAACTGG 3300
Db
3241 ATCGGATGCAATTTGTTGATAATCAGCACTTGGCCATGCTAGCAAGAAACCTTGAACTGG 3300
QY
3301 ATCCATTTATGCTGTATGCTCACGGGCTGACCTTTGTAGAGATCGGACCTTCGACATG 3360
|||||

Db
3301 ATCCATTTATGCTGTATGCTCACGGGCTGACCTTTGTAGAGAAATCGGACCTTCGACATG 3360
QY
3361 CAATGGCCAAATGTTTGAAGCGTTAAATAGAGCTGTTTAACTTTGGAGGAAAGCCCTGGAGG 3420
Db
3361 CAATGGCCAAATGTTTGAAGCGTTAAATAGAGCTGTTTAACTTTGGAGGAAAGCCCTGGAGG 3420
QY
3421 AAGCCAAAGCAGTTAATTTGGAGCGTCTCTTTAATGATCCGACCTGCGGAAAGTCTGGC 3480
Db
3421 AAGCCAAAGCAGTTAATTTGGAGCGTCTCTTTAATGATCCGACCTGCGGAAAGTCTGGC 3480
QY
3481 TCAATTAATCTCTCCACCCACTCCAACTACAAGAGCCAAATACCTGATCGAACAACTTATTG 3540
Db
3481 TCAATTAATCTCTCCACCCACTCCAACTACAAGAGCCAAATACCTGATCGAACAACTTATTG 3540
QY
3541 AAACTTCTCCAGTTCTACAAAACCTTACTGAGTTTGAAGAACAAATTTGGAGTAAATTTTAA 3600
Db
3541 AAACTTCTCCAGTTCTACAAAACCTTACTGAGTTTGAAGAACAAATTTGGAGTAAATTTTAA 3600
QY
3601 CTGATGTTCCGACTTTCTGGCAGGCGATTCATTTGAGAACTGTGGGATTTAAACCATCTGA 3660
Db
3601 CTGATGTTCCGACTTTCTGGCAGGCGATTCATTTGAGAACTGTGGGATTTAAACCATCTGA 3660
QY
3661 CCCTAGGCCCAATCAGAGAAATGGAATTCCTAGGTGACTCCATATGCAACTGGTAGCCA 3720
Db
3661 CCCTAGGCCCAATCAGAGAAATGGAATTCCTAGGTGACTCCATATGCAACTGGTAGCCA 3720
QY
3721 CAGAGTACTTATTCATTTCCAGATCATCATGAAGGACACTTAACTTTGTTGCGAA 3780
Db
3721 CAGAGTACTTATTCATTTCCAGATCATCATGAAGGACACTTAACTTTGTTGCGAA 3780
QY
3781 GCTCTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGGATGCGAGGT 3840
Db
3781 GCTCTTTGGTGAATAATAGAACTCAGGCCAAGGTAGCGGAGGAGCTGGGATGCGAGGT 3840
QY
3841 ACGCCATAAACCAACGACCAAGAGCGCTGTGGCGCTTCGCAACCAAGACCTTTGGCGG 3900
Db
3841 ACGCCATAAACCAACGACCAAGAGCGCTGTGGCGCTTCGCAACCAAGACCTTTGGCGG 3900
QY
3901 ACCTTTTGGAAATCATTTATTCAGCGCTGTACACTGATAGGAATTTGGAATATGTTTCA 3960
Db
3901 ACCTTTTGGAAATCATTTATTCAGCGCTGTACACTGATAGGAATTTGGAATATGTTTCA 3960
QY
3961 CTTTTCATGAATGCTGCTTCTTTCCAGATTTGAAGAAATTCATTTTGAATCAGGATTTGA 4020
Db
3961 CTTTTCATGAATGCTGCTTCTTTCCAGATTTGAAGAAATTCATTTTGAATCAGGATTTGA 4020
QY
4021 ATGACCCCAATCCAGCTTCAGCAGTGTCTTGACACTTAGGACAGAGGAAAGAGC 4080
Db
4021 ATGACCCCAATCCAGCTTCAGCAGTGTCTTGACACTTAGGACAGAGGAAAGAGC 4080
QY
4081 CAGACATTCCTCTGTACAAGACTCTGCAGACAGTGGGCCCATCCCATGCCGAACTTACA 4140
Db
4081 CAGACATTCCTCTGTACAAGACTCTGCAGACAGTGGGCCCATCCCATGCCGAACTTACA 4140
QY
4141 CTGTGGCTGTTTATTTCAAGGAGAAAGATAGGCTGTGGGAAAGGACCAAGTATTCAGC 4200
Db
4141 CTGTGGCTGTTTATTTCAAGGAGAAAGATAGGCTGTGGGAAAGGACCAAGTATTCAGC 4200
QY
4201 AAGCGGAAATGGGAGCAGCAATGGATGCGCTTGAATAATATAATTTTCCAGATGGCCC 4260
Db
4201 AAGCGGAAATGGGAGCAGCAATGGATGCGCTTGAATAATATAATTTTCCAGATGGCCC 4260
QY
4261 ATCAGAAAGCGGTTTATCGAAACGGAAGTACAGACAGAGTTTAAAGAAATGAGGTGGGAAA 4320
Db
4261 ATCAGAAAGCGGTTTATCGAAACGGAAGTACAGACAGAGTTTAAAGAAATGAGGTGGGAAA 4320
QY
4321 GAGAGCATCAAGAGAGAGCCAGATGAGACTGAGACATCAAGAAATAAGAGGCGCAT 4380
Db
4321 GAGAGCATCAAGAGAGAGCCAGATGAGACTGAGACATCAAGAAATAAGAGGCGCAT 4380
QY
4381 GCAAGTGTGAGTATTTACTTGTCTCAGTAACTGTGACTGTGTTGTTGAGACCTGACCT 4440
Db
4381 GCAAGTGTGAGTATTTACTTGTCTCAGTAACTGTGACTGTGTTGTTGAGACCTGACCT 4440


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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3725

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Query Match	1.1%;	Score 54.4;	DB 6;	Length 3649;
Best Local Similarity	47.4%;	Pred. No. 0.00019;		
Matches 163;	Conservative 0;	Mismatches 181;	Indels 0;	Gaps 0;
QY	3109	ATGACCCCAACTCCCTCGAGGATTAACCAACAATGAACGGTTGGAAATTCCTGGGGTGATCGTG	3168	
Db	1787	ATGACCTTTAATATGAATCGTTTAGAACACACAGCAACGCTTAGAATTTTATAGTGATCGCG	1728	
QY	3169	TTGTGGAATTTCTGCACCGCTCCATTTGTGTACTATTTGTCTTAGTCTCGAAGAAGGAG	3228	
Db	1727	TATTAGAATTTGACGGTTTCACGCTATCTTTTGTGCAGACATCCCTCATTTACCAGAAGGTA	1668	
QY	3229	GATTAGCAACCTTATCGGACTGCCATTTGTAGAAATCAGACACTTGTCGCATCGTAGCAAGA	3288	
Db	1667	ATTTGCAACAAGATGCGCGCAACAATTTGTTGTGAACTTTCATCTTGTGATATTTTGCGAATA	1608	
QY	3289	AACTTGAACCTGATCCATTTATGCTGTATGCTCAGGGCCCTGACCTTTGTAGAGAAATCGG	3348	
Db	1607	AGATTAAATTAACGAACCTGATTTTATTAGGTAAAGGTGAAGAGACAGGAGCGCAAGAA	1548	
QY	3349	ACCTTCGACATGCAATGGCCCAATTTTGTGAAGCGTTAAATAGGAGCTGTTTACTTTCGAGG	3408	
Db	1547	CAAGACCTTCCCTTATTCAGATGCAATTTGAAGCTTTGTAGGTGCATGTATTTAGATC	1488	
QY	3409	GAAAGCCTGGAGGAAGCAAGCATTTATTTGGACGGTTGCTCTTTT	3452	
Db	1487	AAAGTTTTAGATTTCAGTATGGACAATTTGCTGAAAAGATCATCTTT	1444	

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RESULT 5
US-11-121-086-18/c
; Sequence 18, Application US/1121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 175023
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-18

Query Match          1.1%; Score 54.2; DB 7; Length 175023;
Best Local Similarity 49.5%; Pred. No. 0.0036;
Matches 140; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY      440  CTCACAGCCCCCAATTTCTCCTCCACGACGAGACTTTGTATCCCTTCCCCCACCACAT 499
          |||
Db       123594  CTCCTCTCTCCCTCCCTCCCTCCCATCCGCTCCCTCCCTCTCTCTCTCTCTCCCTCCCAT 123593

QY      500  GCCTCGTGAAGGCAAGGCCCTCTTCCGCTCGGCCAATCAGGGCGGCTTTCCCAACCA 559
          |||
Db       123534  CCCCCCTCCCTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 123475

QY      560  CCAGATGAGGCACCCCTTCCAGTTCTCTGTGTTTCTTCCCATGCAACCAATGCC 619
          |||
Db       123474  CCCCCTCTCTCCCTCCCTTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 123415

QY      620  TTGTCTCTAATAACCCCCCAGTCCCTGGGGCACTCTCTGGAAGGACCTTTTCCCTTTCAT 679
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Db      123414  CTCTCCCTCCGCTCCGCCCGTCCCGCCCCCCTCTCTCCGCTCCGCTCCCGCTCCGCTCCGCTCT 123355
Qy      680    GATGCCCGCTCCCTCCCATGCCTCATCCCGCGCCCTCCAGTC 722
         |||||
Db      123354  CCTCCCTCCCGCTCCCTTTCCGCTTCCGCTTCCGCTTCCGCTCCCCTC 123312
         |||||

RESULT 6
US-10-996-217A-6/c
; Sequence 6, Application US/10996217A
; Publication No. US2005026561A1
; GENERAL INFORMATION:
;   APPLICANT: Revivicor, Inc.
;   APPLICANT: Wells, Kevin
;   TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Ani
;   FILE REFERENCE: 10785.105070 REV 1015 US
;   CURRENT APPLICATION NUMBER: US/10/996,217A
;   PRIOR FILING DATE: 2004-11-22
;   PRIOR APPLICATION NUMBER: 60/523,938
;   PRIOR FILING DATE: 2003-11-21
;   NUMBER OF SEQ ID NOS: 272
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 6
;   LENGTH: 1557
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-996-217A-6

Query Match          1.1%; Score 53; DB 6; Length 1557;
Best Local Similarity 50.6%; Pred. No. 0.00025;
Matches 128; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

Qy      474    GACTTTGTACCTTCCCCCACCCATGCTCGTCAGGGCAAGGCGCTCTTCCCGCCCTGC 533
         |||||
Db      1495    GTCTTTTTCCTCCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1436
         |||||
Qy      534    CCAATCAGGCGCGCTTTCCTCCCAACCACACAGATGAGGACCCCTTCCAGATTCTCTTGTT 593
         |||||
Db      1435    CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1376
         |||||
Qy      594    TTTTCTCCCATGCACACCAAATGCTTGTCTTAATAACCCCCCAGTCCCTGGGGCAGCT 653
         |||||
Db      1375    CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1316
         |||||
Qy      654    CTGTGGAAGGCACTTTTCCTTTCATGATGCCGCTCCCTTCCATGCTCATGCCCGGCC 713
         |||||
Db      1315    CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1256
         |||||
Qy      714    CTCCTCAGTCATGC 726
         |||||
Db      1255    CTTCTGTGTAATAC 1243
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RESULT 7
US-11-121-086-2
; Sequence 2, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138. 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 191684
; TYPE: DNA

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; ORGANISM: Homo sapiens

US-11-121-086-2

Query Match 1.1%; Score 53; DB 7; Length 191684;

Best Local Similarity 50.5%; Pred. No. 0.0084;

Mismatches 156; Conservative 0; Mismatches 150; Indels 3; Gaps 1;

QY 412 CAAGTGCGCCCTTCACACATTTTCAAACTCTCAGGCCGCCCAGATTCTCCCTCCACGCAC 471

DB 71460 CCACTGGCCCTCCAGCCCTTCCACTGCCCCACTCCGCCACCCTGCCCCCTTCTCTCCCTCC 71519

QY 472 CAGACTTGTACCTTCCCGCCACCATGCTCCGTCAGCGCAAAGGCCCTCTTCC---CC 528

DB 71520 ACTTCCCTCTTCCCTCCCTCTTCCCTCTCTCTCCGCGCTGCCCTTCCCTTCCCTCC 71579

QY 529 CCTGCCCCAATCAGGCGGCTTTCCTCCCAACAACAGAGGAGCACCGCTTCCAGTTCCTC 588

DB 71580 ACTGCCACATCCCCACCCCTGCGCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTC 71639

QY 589 CTGTGTTTTCTCCATGCGACGACCAATGCTTGTCTTAATAACCCCGCCAGTCCCTGGSG 648

DB 71640 TCTCTCTCCCTCCCTCCACCGCCACTCCCTCCGCTGCTCCCGCTCCCTTCCCTT 71699

QY 649 CACCTCTGTGAAGGACATTTCCCTTTCATGATGCCCCCTCCCTCCATGCTTCATFCCC 708

DB 71700 CCCCTCCCTCTCCCTCAGCTGCGCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTC 71759

QY 709 CGCCCTCTC 717

DB 71760 ACTGCCAC 71768

RESULT 8

US-11-074-176-135

; Sequence 135, Application US/11074176

; Publication No. US20050250135A1

; GENERAL INFORMATION:

; APPLICANT: Klaenhammer, Todd R.

; APPLICANT: Russell, William M.

; APPLICANT: Altermann, Eric

; APPLICANT: McAulliffe, Olivia

; APPLICANT: Peril, Andrea Azcarate

; TITLE OF INVENTION: Nucleic Acid Sequences Encoding

; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore

; FILE REFERENCE: 5051-694

; CURRENT APPLICATION NUMBER: US/11/074,176

; CURRENT FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: 60/551,161

; PRIOR FILING DATE: 2004-03-08

; NUMBER OF SEQ ID NOS: 381

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 135

; LENGTH: 684

; TYPE: DNA

; ORGANISM: Lactobacillus acidophilus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(684)

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (0)..(0)

; OTHER INFORMATION: ORF 1297; Ribonuclease III

US-11-074-176-135

Query Match 1.1%; Score 51.2; DB 7; Length 684;

Best Local Similarity 47.3%; Pred. No. 0.00045;

Mismatches 155; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

QY 3109 ATGACCCAATCCCTCGAGGATTAAACCAATGAACGGTGTGAATTCTCTGGGTGATGTG 3168

DB 104 ATGAACATCTCTGATGATGGGATTCGTGATTATGAAGAATTAGAGTTCCTTAGGTGATG 163

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US-10-353-361-13458

Query Match          1.0%; Score 46.8; DB 6; Length 36360;
Best Local Similarity 46.8%; Pred. No. 0.14;
Matches 147; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

QY      409 CTCCAAGTGGCCCTTCACCATCTTTCAAATCTCGAGGCCGCAATTTCTCCGTCCAC 468
Db      22209 TCCCCCTCTCCTCCTCTCTCTCCTCCCTCCCTCTCTCTCCACCTACTCTCTCCCCCGCTCCCT 22150
QY      469 GACCAGACTTTGTACCCCTTTCGCCCCACACCATGCCTCCGTCAGAGGCAAGGCCCTCTTCCC 528
Db      22149 CCGTCCCTCTTTTCCCTCTCCTCTCTCTCCCTCTCTCTCCCTCTCTCCCTCTCTCCCTC 22090
QY      529 CTGTCCCAATCAGGGCGCGCTTTCCCAACACACAGATGAGGCACCCCTTCCCAGTTCCTC 588
Db      22089 CCCTTTCCCTCTCCTCCCTCTCCCTCTCCCTCTCTCTCCCTCTCCCTCTCTTTCCTCC 22030
QY      589 CTGTGTTTCTCCCATGCGCACACAATGCTTGTCCTAATAACCCCCCAGTCCCTGGGG 648
Db      22029 TCCTCTCTCTCCCGCTCTCTCCCTCTGTCTCCCTCTCTCTCCCTCTCTCTCCCTCTCTCT 21970
QY      649 CACCTCTCGGAGAAGGCATTTCCTCCCTTCATGATGCGCCCTCCCTCCCATGCTCATCCCC 708
Db      21969 CTCTGTCTCTCCCTCCCTCTCTCTCCCTCTCTCTCCCTCTCTCTCCCTCTCTCTCCCT 21910
QY      709 CGCCCCCTCCAGTC 722
Db      21909 TCCTCCCTCCCTC 21896

RESULT 12
US-11-097-728-1
; Sequence 1, Application US/11097728
; Publication No. US20050260132A1
; GENERAL INFORMATION:
; APPLICANT: Erik Foehr
; APPLICANT: Sabine Muller
; APPLICANT: Daniel J. Chin
; APPLICANT: Mirella Gonzalez-Zulueta
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES DIRECTED TO RECEPTOR PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASE ZETA
; FILE REFERENCE: AGYT-006CIP
; CURRENT APPLICATION NUMBER: US/11/097,728
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: 10/652,981
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 7941
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148) ... (7092)
US-11-097-728-1

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; NAME: AG1; CDS
; LOCATION: (148)...(7092)
US-11-097-728-1

Query Match      1.0%; Score 46.2; DB 7; Length 7941;
Best Local Similarity 49.4%; Pred. No. 0.069;
Matches 120; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 4522 GTTTTTAGCTGGATGGCTCTTTATTACAAAGTATTAGATTTTTCTCTATTATTAAACGGAAAA 4581
Db 7693 GTAGTTTCATTAGCTGGCTTACTACACAGTTTCTGCACATTGTTGTGTACCTAAGT 7752
QY 4582 CTTGACTTTGGTGAATGTCATTACTTCCTTTTATTTTGCTCTTTAAATAATAAATTCA 4641
Db 7753 CATTAACTTTGTTTCAGCATGTAATTTTAACTTTTGTGGAAAATAGAAATACCTTCATTT 7812
QY 4642 AGAAGCATATTCTATGTGGAAATAGATCCTGTTTTTCCATCTGTGTCACGATTTGTGACC 4701
Db 7813 TGAAGAAGAAGTTTTTATGAGATAACACCTTACCAAAACATTTGTTCAAATGGTTTTTATATCCA 7872

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; LOCATION: (825401)
; OTHER INFORMATION: the 'n' at position 825401 may be 'c' or 'a'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (825428)
; OTHER INFORMATION: the 'n' at position 825428 may be 'g' or 'a'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (825473)
; OTHER INFORMATION: the 'n' at position 825473 may be 'g' or 'a'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (825765)
; OTHER INFORMATION: a "c" may be deleted at this position
; FEATURE:
; NAME/KEY: allele
; LOCATION: (825828)
; OTHER INFORMATION: the 'n' at position 825828 may be 'c' or 't'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (826041)
; OTHER INFORMATION: the 'n' at position 826041 may be 'a' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (826546)
; OTHER INFORMATION: the 'n' at position 826546 may be 'a' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (826654)
; OTHER INFORMATION: the 'n' at position 826654 may be 'a' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (826826)
; OTHER INFORMATION: the 'n' at position 826826 may be 'a' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (826863)
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; NAME/KEY: allele
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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2005, 14:23:08 ; Search time 23208 Seconds
(without alignments)
11668.485 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba.*
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15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4760.8	99.9	4764	6 CS042637	Sequence
4	4760.8	99.9	4764	8 AF189011	Homo sapi
5	4343.4	91.2	4650	8 HSM807870	Sequence
6	3600	75.6	4069	8 BC054003	Homo sapi
7	3379.6	70.9	4479	9 BC088999	Mus muscu
8	3042.2	63.9	3838	9 BC060265	Mus muscu
9	2582	54.2	2598	6 BD155916	Primer fo
10	2582	54.2	2598	6 AX876043	Sequence
11	2582	54.2	2598	6 AK001121	Homo sapi
12	2564	53.8	4516	5 AJ720721	Gallus ga
13	2525.2	53.0	2607	8 BC024261	Homo sapi
14	2442	51.3	2473	8 BC041162	Homo sapi
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21	1744	36.6	2229	9 BC040801	Mus muscu
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ALIGNMENTS

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LOCUS AR540925 4764 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1 from patent US 6737512.
ACCESSION AR540925
VERSION AR540925.1 GI:53932478
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4764)
AUTHORS Wu,H. and Crooke,S.T.
TITLE Human RNase III and compositions and uses thereof
JOURNAL Patent: US 6737512-A 1 18-MAY-2004;
ISIS Pharmaceuticals, Inc.; Carlebad, CA
FEATURES
source location/Qualifiers
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/organism="unknown"
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ORIGIN

Query Match	100.0%;	Score 4764;	DB 6;	Length 4764;
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ACCESSION CS033685
VERSION CS033685.1 GI:60732625
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominoidea; Homo.

REFERENCE
1 Abbas, A., Clark, H., Ouyang, W., Williams, M. P., Wood, W. I. and Wu, T. D.
AUTHORS Compositions and methods for the treatment of immune related
TITLES diseases
JOURNAL Patent: WO 2005016962-A 3191 24-FEB-2005;
Genentech, Inc. (US)
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LOCUS CS042637 4764 bp DNA linear PAT 22-MAR-2005
DEFINITION Sequence 3191 from Patent WO2005019258.
ACCESSION CS042637
VERSION CS042637.1 GI:61849798
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominidae; Homo.
REFERENCE 1
AUTHORS Abbas, A., Clark, H., Ouyang, W., Williams, P.M., Wood, W.I. and Wu, T.D.
TITLE Compositions and methods for the treatment of immune related diseases
JOURNAL Patent: WO 2005019258-A 3191 03-MAR-2005;
Genentech, Inc. (US)
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10948199
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 Xu, H., Wu, H., Miraglia, L. J. and Crooke, S. T.
 Direct Submission
 Submitted (22-SEP-1999) Structural Biology, ISIS Pharmaceuticals,
 2292 Faraday Avenue, Carlsbad, CA 92008, USA
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Db	4681	CTGTGTCCTCCAGATTGTGACCTAGACCTTTCAATTGACAGTAAATAAATTTGACTTTACTTAG	4740
Qy	4741	TAAAAAATAAAAAAAAAAAAAAAAAAAAAA	4764
Db	4741	TAAAAAATAAAAAAAAAAAAAAAAAAAAAA	4764
RESULT 5			
LOCUS	HSMB07870	4650 bp mRNA linear	PRI 30-AUG-2003
DEFINITION	Homo sapiens mRNA; cDNA DKFZp686F16262 (from clone DKFZp686F16262).		
ACCESSION	BX647724		
VERSION	BX647724.1	GI:34366881	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 4650) Poustka.A., Albert.R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.		
CONSRMT	The German Human cDNA Consortium		
TITLE	Direct Submission		
JOURNAL	Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Nuherberg, GERMANY		
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686F16262) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.		
FEATURES	Location/Qualifiers		
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	/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host: DH10B; sites SfiI + SfiII"		
	/dev_stage="adult"		
polyA_signal	4613..4618		
polyA_site	4629		
ORIGIN			
Query Match	91.2%;	Score 4343.4;	DB 8; Length 4650;
Best Local Similarity	97.3%;	Pred. No. 0;	
Matches 4471; Conservative	0; Mismatches	11; Indels	111; Gaps 1;
Qy	58	GAGAGCCTTTATAGGTTGCTTTTCCCGGGATGTGAAGGATACAGAAATGACTGTCAAT	117
Db	151	GAGTACTTTTCAGGTTGCTTTTCCCGGGATGTGAAGATACAGAAATGACTGTCAAT	210
Qy	118	CAACCCATATCATCAAGAGGCTGATAATCTAGTGGAGAGTTAGACTGTGCATCTTCA	177
Db	211	CAACCCATATCATCAAGAGGCTGATAATCTAGTGGAGAGTTAGACTGTGCATCTTCA	270
Qy	178	CTATGATATGAGGAGTCTCTGAGCTTATATCTCTGTGGAAGATGTGACATATCCAGGC	237
Db	271	CTATGATATGAGGAGTCTCTGAGCTTATATCTCTGTGGAAGATGTGACATATCCAGGC	330
Qy	238	GGAAACATCATGTATGAGGGGAAACACATGTCCACAGATGTCTGTTCCACCCGGGACGAGGC	297
Db	331	GGAAACATCATGTATGAGGGGAAACACATGTCCACAGATGTCTGTTCCACCCGGGACGAGGC	390
Qy	298	GTCCCCGAGGACGAGGAGCATGTGGAGCCAGACCCCTCAGACCCATCTCTTAGGCCCCAAA	357

Db 391 GTCCCGAGGACGAGGAGACATGGAGCCAGACCCCTCAGACCACTCTTTAGGCCCCAAA 450
QY 358 ATCTGAGGCTGTTTCAACCTCAGCAGCCTCTGTGCAATATCAATATGAACCTCCAGTG 417
Db 451 ATCTGAGGCTGTTTCAACCTCAGCAGCCTCTGTGCAATATCAATATGAACCTCCAGTG 510
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Db 1051 ATGGGCGAGTGAGGCACTCGTCTCCGTGATCGCGGAGCGAGCCCGCAGTCCGACA 1110
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Db 1111 GGAGAGACAAGACAGCCGGTACAGATCTGATTATGACCGAGGGAGAACCAATCTCGCC 1170
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Db 1286 ----- 1285
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RESULT 6

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Db 4600 TTGCTCTTTTAAATAATAAATTTCAAGAGCATATA 4632

BC054003	4069 bp	mrna	linear	PRI 20-MAY-2005
LOCUS				
DEFINITION	Homo sapiens ribonuclease III, nuclear, mRNA (cdna clone MGC:61568 IMAGE:6148714), complete cds.			
ACCESSION	BC054003			
VERSION	BC054003.1	GI:32450505		
KEYWORDS	MGC.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 4069)			
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Ustin,T.B., Toshituki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kerteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.			
CONSRMTM	Mammalian Gene Collection Program Team			
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
PUBMED	12477932			
REFERENCE	2 (bases 1 to 4069)			
AUTHORS	NIH MGC Project			
CONSRMTM	Direct Submission			
JOURNAL	Submitted (24-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA			
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov			
COMMENT	Contact: MGC help desk Email: cgaps@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTF cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@hghri.nih.gov Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Leric,P., Legaspi,R., Maduro,Q.L., Masello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantropop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.			
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 115 Row: 1 Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21359821.			
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IMAGE:6417566), complete cds.
ACCESSION BC088999
VERSION BC088999.1 GI:57242919
SOURCE MGC.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4479)
AUTHORS Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altechul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Sheets,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahney,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schmerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
CONSRMT Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
AUTHORS 2 (bases 1 to 4479)
CONSRMT NIH MGC Project
TITLE Direct Submission
JOURNAL Submitted (06-JAN-2005) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Thomas L. Casavant.
Web site: <http://genome.uiowa.edu>
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fisher,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Schetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: Plate: Row: Column: 0
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

FEATURES
source

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ORIGIN

Query Match 70.9%; Score 3379.6; DB 9; Length 4479;
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QY 4288 ACAGACAGAGTTAAAGAAATAGGTGGGAAGAGAGCATCAAGAGAGAGAGCCAGATG 4347

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RESULT 8

LOCUS BC060265

DEFINITION Mus musculus ribonuclease III, nuclear, mRNA (cdna clone IMAGE:5698108), partial cds.

ACCESSION BC060265

VERSION BC060265.1

KEYWORDS GI:37994703

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3838)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wernley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.B., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Mammalian Gene Collection Program Team

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 3838)

NIH MGC Project

Direct Submission

Submitted (20-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs@mail.nih.gov

Tissue procurement: Dr. Jim Lin, University of Iowa

cDNA Library Preparation: M. Bento Soares, University of Iowa

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Martin Hirat, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Mabel Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR Santos, Duane Smalus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC plate: 132 Row: a Column: 17

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

Location/Qualifiers

1. 3838

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/clone="IMAGE:5698108"

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<1. 3697

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gene

source

CDS

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ERSYKEYKRSYALVPAPEPACTPELPGEMIKTTPESWAPPENVHRSPSPREK
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ORIGIN

Query Match		63.9%;	Score 3042.2;	DB 9;	Length 3838;
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Matches 3355;		Conservative	0;	Mismatches 458;	Indels 8; Gaps 3;
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Qy	734	GGTTAATTATCAGTACCTCCGGGCTATTCTCACCACAACTTCCACCTCCCGATTTTAA	793		
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KEYWORDS	JP 2002191363-A/10759.
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 2598)
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE	Primer for synthesizing full-length cDNA and use thereof
JOURNAL	Patent: JP 2002191363-A 10759 09-JUL-2002;
COMMENT	HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191363-A/10759 PD 09-JUL-2002 PF 28-JUL-2000 JP 2000280990 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO, PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC 10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC Primer for synthesizing full-length cdna and use thereof FH Key Location/Qualifiers (10)..(2316).
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source	1..2598 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
ORIGIN	Query Match 54.2%; Score 2582; DB 6; Length 2598; Best Local Similarity 99.6%; Pred. No. 0; Matches 2588; Conservative 0; Mismatches 10; Indels 0; Gaps 0; Qy 2052 GGATTTTCTATGTTTCACATGCCCCCTGCACCAATATTTCCACTGTGTAAAGTAATTAGA 2111 Db 1 GGATTTTCTATGTTTGACATGCCCCCTGCACCAATATTTCCACTGTGTAAAGTAATTAGA 60 Qy 2112 TTCAAATACATGATACAGGATTCATTTTCATTTGAAGAGATGATGCCGGAGAAATTTTGTGTG 2171 Db 61 TTCAAATACATGATACAGGATTCATTTTCATTTGAAGAGATGATGCCGGAGAAATTTTGTGTG 120 Qy 2172 AAGGGCTTGAATCTTTTCACTGTTCTATTTACAGATATATTTTGAATATATGACTGG 2231 Db 121 AAGGGCTTGAATCTTTTCACTGTTCTATTTACAGATATATTTTGAATATATGACTGG 180 Qy 2232 AATCTTAAAGGTCCTTTTGTGAAGCACGCCCTCCCTGCTGCCCAAGATTTTCATTTCATG 2291 Db 181 AATCTTAAAGGTCCTTTTGTGAAGCACGCCCTCCCTGCTGCCCAAGATTTTCATTTCATG 240 Qy 2292 CCACGTTTTGTAAAGATTTCTTCCAGATGGAGAAAGAGTAGTCTGTCCATGCCACAGATT 2351 Db 241 CCACGTTTTGTAAAGATTTCTTCCAGATGGAGAAAGAGTAGTCTGTCCATGCCACAGATT 300 Qy 2352 CTCCTGTACTTTGTAAGGTGCAGAAAGCCCTGGTGCCTGAGGAGAGATTTGCCAATATG 2411 Db 301 CTCCTGTACTTTGTAAGGTGCAGAAAGCCCTGGTGCCTGAGGAGAGATTTGCCAATATG 360 Qy 2412 CTTTCAGTGGGAGAGCTGGAGTGGCGAATAATGACAGAGATGCAAAAGGCATGATTTGTT 2471 Db 361 CTTTCAGTGGGAGAGCTGGAGTGGCGAATAATGACAGAGATGCAAAAGGCATGATTTGTT 420 Qy 2472 ACCAACCTGGGACGAAACCAGACTCTGTCCGTATCGATCAACTGGATCGTGAACAGTTTC 2531 Db 421 ACCAACCTGGGACGAAACCAGACTCTGTCCGTATCGATCAACTGGATCGTGAACAGTTTC 480 Qy 2532 AACCCCAGATGTATTTACTTTTCGGATATTCGTCCAATTTGGGATACGCCCTGCAAGTTG 2591 Db 481 AACCCCAGATGTATTTACTTTTCGGATATTCGTCCAATTTGGGATACGCCCTGCAAGTTG 540

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RESULT 10
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LOCUS AX876043 2598 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 10948 from Patent EP1074617.

AX876043
AX876043.1 GI:40030779
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Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1
Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.,
Primers for synthesising full-length cDNA and their use
Patent: EP 1074617-A 10948 07-SEP-2001;
Research Association for Biotechnology (Jp)
LOCATION/Qualifiers
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ORIGIN

Query Match 54.2%; Score 2582; DB 6; Length 2598;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2052 GGATTTTCTATGTTTGACATGCCCCCTTGACCAATATTCCACTGTGTAAAGTAATAGA 2111
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RESULT 11

AK001121

LOCUS

DEFINITION

to Homo sapiens cDNA FLJ10259 fis, clone HEMBB1000947, highly similar

to Homo sapiens clone HAW100 putative ribonuclease III mRNA.

AK001121

ACCESSION

VERSION

KEYWORDS

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

1

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AUTHORS

Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,

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Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,

Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,

Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,

Shiratori, A., Sudo, H., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H.,

Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,

Kikawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,

Tanikawa, M., Yamazaki, M., Ninomiya, K., Iehibashi, T., Yamashita, H.,

Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M.,

Hirooka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,

Yosida, M., Tanase, T., Kusano, J., Kanehori, K., Takahashi, F.,

Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R.,

Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A.,

Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,

Shiohata, N., Sano, S., Mori, S., Momiya, H., Sato, N., Takami, S.,

Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,

Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,

Kumagai, A., Itakura, M., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,

Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y.,

Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hiki, J., Kobatake, N.,

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Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K.,

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Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,

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Complete sequencing and characterization of 21,243 full-length

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Nat. Genet. 36 (1), 40-45 (2004)

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Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,

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Wagatsuma, M., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H.,

Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,

Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,

Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,

Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.

NEDO human cDNA sequencing project

Unpublished

3 (bases 1 to 2598)

Isogai, T. and Otsuki, T.

Direct Submission

Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,

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(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

International Trade and Industry of Japan; cDNA full insert

sequencing: Research Association for Biotechnology; cDNA library

construction, 5'- & 3'-end one pass sequencing and clone selection;

Helix Research Institute (supported by Japan Key Technology Center

etc.) and Department of Virology, Institute of Medical Science,

University of Tokyo.

Location/Qualifiers

FEATURES

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LOCUS
DEFINITION
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IMAGE:3631271).
ACCESSION
BC024261
VERSION
BC024261.1 GI:22028101
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 2607)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P.,
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Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
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Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 2607)
NIH MGC Project
Direct Submission
Submitted (26-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR
Santos, Duane Smalls, Jeff Stott, Miranda Tsai, George Yang,
Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found
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DEFINITION Homo sapiens ribonuclease III, nuclear, mRNA (cDNA clone
IMAGE:5114643), partial cds.

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ACCESSION BC041162
VERSION    BC041162.1 GI:27552889

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KEYWORDS

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SOURCE     Homo sapiens (human)

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ORGANISM

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

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REFERENCE
AUTHORS    Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altshul,S.P., Zeeberg,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932

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REFERENCE

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2 (bases 1 to 2473)

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AUTHORS

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NIH MGC Project
Direct Submission
Submitted (16-DEC-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov

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REMARK

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COMMENT
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org

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Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

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Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 84 Row: c Column: 15.
Location/Qualifiers

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ORIGIN

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Query Match      51.3%; Score 2442; DB 8; Length 2473;
Best Local Similarity 99.8%; Pred. No. 0;
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Qy      2261  CCCTCCCTCTGCCCAAGATTTCAATTCATGCCACGCTTTTGAAGATTTCTTCCAGATGG 2320
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Db	121	AGGAAAGGAAGTGTCTCCATGCACACAGATTCTCCTGTACTTGTAAAGGTGCAGCAAGC	180
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Db	241	ATATGCAGAAAGATGCAAAGGAGATGATTGTATACCAACCCCTGGGAGCAAAACCAAGCTCTGT	300
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Db	301	CGGTATCGATCAACTGGATCGTGAACAGATTCAACCCCGATGTGATTACTTTTCCGATTAT	360
Qy	2561	CGTCCACTTTGGGATAGCCCTTCGACAGTTGAGTTATGACAGAGACCCACAGTACCAAAA	2620
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Qy	3341	AGAACTCGGACCTTCGACATGCAATGCCAATTTGTTTGAAGCGTTAATAGGAGCTGTTTA	3400
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ACCESSION BC057687
VERSION BC057687.1 GI:34784427
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SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2971)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 2971)
NIH MGC Project
Direct Submission
Submitted (03-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapsb-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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Db 2462 ATTCTGATCAGATTTGGAACGCCCAAGTCCGAGCTGACAGAGTGTGCTGACCTG 2521
QY 4062 AGGACAGAAAGGAAAGAGCCAGATTTCTCTGTACAGACTCTGACAGACAGTGGGCCCA 4121
Db 2522 AGGACAGAAAGGAAAGAGCTGACATCCCTTTATACAGACTCTGACAGACAGTGGGGCCA 2581

```
QY 4122 TCCATGCCCGAACCTACACTGTGGCTGTTTATTTCAAGGGAGAAAGAAATAGGCTGTGGG 4181
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2582 TCCATGCTAGAACCTACACTGTGGCTGTTTATTTCAAGGGAGAAAGAAATAGGCTGTGGG 2641
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4182 AAAGGACCAAGTATTTCAGCAAGCGGAAATGGGAGCAGCAATGGATGCGCTTGAAAAATAT 4241
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2642 AAAGGACCAAGCATTCAGCAGCGCGGAGATGGGAGCAGCAATGGATGCGCTGGAGAAATAT 2701
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4242 AATTTTCCCGAGATGGCCCATCAGAACCGGTTTCATCGAACCGGAAGTACAGACAAGAGTTA 4301
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2702 AACTTTCCCGAGATGGCCCATCAGAACCGGTTTCATCGAACCGGAAGTACAGACAAGAGTTA 2761
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4302 AAAGAAATGAGGTGGGAAAGAGAGCATCAAGAGAGAGAGCCAGATGAGACTGAAGACATC 4361
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2762 AAGGAATGAGGTGGGAAAGAGAGCATCAGAGAGAGAGCCGAGGAGGCTGAAGACATC 2821
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4362 AAGAAATAAGGAGGCGCATGCAAGTGTGGAGTATTTACTTGTCTCAGTAACTGTGACTGTT 4421
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2822 AAGAGTAAAGGAGGCGCAGG--AGTGGCGGAGCATTTGCCCTTCTAAGNACTGTGACTGTG 2879
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4422 GTCTATTGAGACCTAGCCTAGTTTCTCTGCAGACAATGAACGAAGTGTGCTCATTTGAAAT 4481
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2880 GCCCATCGAGACCTAGCCTGGTTTCCCTTAGACAATGAATGAAGTGTGCCCATTTGAAAT 2939
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4482 AAAATACAGA 4491
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2940 AAAACTCAAA 2949
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: December 26, 2005, 22:22:23
Job time : 23229 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 24, 2005, 00:37:50 ; Search time 265 Seconds
(without alignments)
3658.098 Million cell updates/sec

Title: US-10-774-974-2

Perfect score: 7500

Sequence: 1 MMQNTCHRMSTFPGRCPR.....MRWERHQREPDTEIDIKK 1374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	NC	Score	Query Match	Length	DB	ID	Description
1	7471	99.6	1374	1	RNC_HUMAN	Q9nr4	homo sapien
2	7160	95.5	1373	2	Q5HZJ0_MOUSE	Q5hzj0	mus musculus
3	6380	85.1	1231	2	Q6PAJ6_MOUSE	Q6paj6	mus musculus
4	6344.5	84.6	1336	2	Q5ZIR3_CHICK	Q5zir3	gallus gall
5	5217	69.6	1021	2	Q80Z69_MOUSE	Q80z69	mus musculus
6	4982	66.4	942	2	Q6P88_MOUSE	Q6p88	mus musculus
7	4121	54.9	780	2	Q7TM18_MOUSE	Q7tm18	mus musculus
8	3767	50.2	1041	2	Q4SKW1_TETNG	Q4skw1	tetraodon n
9	3696	49.3	705	2	Q80U05_MOUSE	Q80u05	mus musculus
10	2963	39.5	1327	2	Q9XYN5_DROME	Q9xyn5	drosophila
11	2881.5	38.4	979	2	Q5TOK8_ANOGA	Q5tok8	anopheles g
12	2825	37.7	541	2	Q8CJ74_MOUSE	Q8cj74	mus musculus
13	2811.5	37.5	1071	2	Q960Y4_DROME	Q960y4	drosophila
14	2683.5	35.8	836	2	Q7PNE9_DROME	Q7pne9	anopheles g
15	2298	30.6	432	2	Q59FF9_HUMAN	Q59ff9	homo sapien
16	1480	19.7	288	2	Q67B98_RAT	Q67b98	rattus norv
17	1473.5	19.6	1061	2	Q61XX9_CAEBR	Q61xx9	caenorhabdi
18	1448	19.3	1086	1	RNC_CAEEL	Q01326	caenorhabdi
19	1154.5	15.4	290	2	Q4SKW3_TETNG	Q4skw3	tetraodon n
20	1138.5	15.2	412	2	Q9CYM4_XENLA	Q9cym4	xenopus lae
21	711	9.5	134	2	Q55FS1_MOUSE	Q55fs1	mus musculus
22	344.5	4.6	230	2	Q82ZG1_ENTFA	Q82zg1	enterococcu
23	340.5	4.5	1150	2	Q8IMM6_DROME	Q8imm6	drosophila
24	340	4.5	846	2	Q8MRP6_DROME	Q8mrp6	drosophila
25	340	4.5	1109	2	Q9VAY4_DROME	Q9vay4	drosophila
26	339	4.5	1389	2	Q55FS1_DICDI	Q55fs1	dictyosteli
27	331	4.4	1838	2	Q6BCJ9_TETTH	Q6bcj9	tetrahymena
28	329.5	4.4	2869	2	Q60PD2_CAEBR	Q60pd2	caenorhabdi
29	328	4.4	1022	2	Q4SPX9_TETNG	Q4spx9	tetraodon n
30	325	4.3	551	2	Q8BX18_MOUSE	Q8bx18	mus musculus
31	321	4.3	249	2	Q65UQ5_BACLD	Q65uq5	bacillus li

RESULT 1

ID	RNC_HUMAN	STANDARD;	PRT;	1374 AA.
AC	Q9NR44; Q7Z5V2; Q86YH0; Q9NW73; Q9Y2V9; Q9Y4Y0;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Ribonuclease III (EC 3.1.26.3) (RNase III) (Drosha) (p241).			
GN	Name=RNASE3L; Synonyms=RN3;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [ISOFORM 1].			
RX	MEDLINE=20538440; PubMed=10948199; DOI=10.1074/jbc.M005494200;			
RA	Wu H., Xu H., Miraglia L.J., Crooke S.T.;			
RT	"Human RNase III is a 160-kDa protein involved in preribosomal RNA processing.";			
RL	J. Biol. Chem. 275:36957-36965(2000).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE OF 166-613 (ISOFORM 2).			
RC	TISSUE=Colon;			
RX	MEDLINE=20431278; PubMed=10976766; DOI=10.1023/A:100717623283;			
RA	Gunther M., Laithier M., Brisson O.;			
RT	"A set of proteins interacting with transcription factor Sp1 identified in a two-hybrid screening.";			
RL	Mol. Cell. Biochem. 210:131-142(2000).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 603-1374.			
RC	TISSUE=Embryo;			
RX	PubMed=14702039; DOI=10.1038/ng1285;			
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,			
RA	Wakamatsu A., Hayashi K., Sato H., Negai K., Kimura K., Makita H.,			
RA	Sekine M., Ohyasui M., Nishi T., Shibahara T., Tanaka T., Ishii S.,			
RA	Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,			
RA	Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,			
RA	Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,			
RA	Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,			
RA	Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,			
RA	Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa M.,			
RA	Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,			
RA	Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotta T.,			
RA	Kusano J., Kanehori K., Takahashi-Fuji A., Hara H., Tanase T.-O.,			
RA	Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,			
RA	Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,			
RA	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,			
RA	Moriya S., Moniyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,			
RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,			
RA	Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,			
RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,			
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,			
RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,			

Q8bx86 mus musculus
Qenvf9 mus musculus
Q7s9h3 neurospora
Q5nv88 pongo pygma
Q53es1 homo sapien
Q16630 homo sapien
P51833 bacillus su
Q4sq65 tetraodon n
Q6ddw4 xenopus lae
Q5z134 gallus gall
Q7xq14 oryza sativ
Q819v8 bacillus ce
Q8y691 listeria mo
Q81w18 bacillus an

DR SMART; SM00358; DSRM; 1.
DR SMART; SM00355; RIBOC; 2.
DR PROSITE; PS00137; DS RBD; 1.
DR PROSITE; PS00517; RNASE 3_1; 2.
DR PROSITE; PS00142; RNASE 3_2; 2.
FT NON TER 1 1_2;
SQ SEQUENCE 1231 AA; 143573 MW; 3679FA9D87800151 CRC64;

Query Match 85.1%; Score 6380; DB 2; Length 1231;
Best Local Similarity 96.1%; Pred. No. 2.9e-303;
Matches 1184; Conservative 22; Mismatches 24; Indels 2; Gaps 2;

QY 144 FMPPPSMPHPPPPVPMQVQVPGYSHHPPPPSPNSFQNNPSSFLPSANNSSPH 203
DB 1 FMVPPPSMPHPPPPVPMQVQVPGYSHHPPPPSPNSFQNNPSSFLPSANNSSPH 59

QY 204 FRLLPPVLPKAPERSRPERLKHDDHRRDHSRGRHRSLDRRERGRSPDRRRODS 263
DB FRLLPPVLPKAPERSRPERLKHDDHRRDHSRGRHRSLDRRERGRSPDRRRODS 119

QY 264 RYRSDYDRGRTPSRHRSYRSRERERHRRDNRSPSLERSYKKEYKRSGRSYGLSV 322
DB RYRSDYDRGRTPSRHRSYRSRERERHRRDNRSPSLERSYKKEYKRSGRSYGLSV 179

QY 323 VPFPAGCTPELPGEIKNTDUSWAPPLEIVNHRSPSRKPKARWEEKDRWSDNQSGDK 382
DB VPFPAGCTPELPGEIKNTDUSWAPPLEIVNHRSPSRKPKARWEEKDRWSDNQSGDK 239

QY 383 NYTSIKEKEPEETMPDKNEEEBELLPVWIRCTHSENYSSDPMDQVGDSTVVGTSRLR 442
DB NYTSIKEKEPEETMPDKNEEEBELLPVWIRCTHSENYSSDPMDQVGDSTVVGTSRLR 299

QY 443 DLYDKFEEELSGRQEKAKAARPPWPKTKLDLEDSESSSECESEDSTCSSSDSEVF 502
DB DLYDKFEEELSGRQEKAKAARPPWPKTKLDLEDSESSSECESEDSTCSSSDSEVF 359

QY 503 DVIAEIKRKAHPDRHLDELWYNDPGQMDGPKCKCSAKARTGIRHSIYPGBEAKPCR 562
DB DVIAEIKRKAHPDRHLDELWYNDPGQMDGPKCKCSAKARTGIRHSIYPGBEAKPCR 419

QY 563 PMTNAGRLPHYRTVSPPTNFLETDRTVLEYDDHEVIFEGSFMAHAPLTNPLCKVIR 622
DB PMTNAGRLPHYRTVSPPTNFLETDRTVLEYDDHEVIFEGSFMAHAPLTNPLCKVIR 479

QY 623 FNIDYTHFTEEMPNFCKVGLFSLFLFRDILEYDNLKGLFEDSPPCPFHFM 682
DB FNIDYTHFTEEMPNFCKVGLFSLFLFRDILEYDNLKGLFEDSPPCPFHFM 539

QY 683 PRFVFLPDGKGVLSMHQILLYLLRCSKALVPEEETANMLQWEELEWQYAECKGMIV 742
DB PRFVFLPDGKGVLSMHQILLYLLRCSKALVPEEETANMLQWEELEWQYAECKGMIV 599

QY 743 TNFGTKPSSVRIDQDREQNPVDVITPIIVHGIRPAQLSYAGDPQYQKLWKSYYKLRH 802
DB TNFGTKPSSVRIDQDREQNPVDVITPIIVHGIRPAQLSYAGDPQYQKLWKSYYKLRH 659

QY 803 LLANSKPVKTDOKLAOREALQKIRQKNTMRREVTVLSSQGFWTKGIRSDVCOHAMM 862
DB LLANSKPVKTDOKLAOREALQKIRQKNTMRREVTVLSSQGFWTKGIRSDVCOHAMM 719

QY 863 LPVLTHIRYHQCLMHLDKLIGYTFQDRCLQLLAWTHPSHLNFGMNPDRHARNSLNCGI 922
DB LPVLTHIRYHQCLMHLDKLIGYTFQDRCLQLLAWTHPSHLNFGMNPDRHARNSLNCGI 779

QY 923 RQPKYGRKVVHMRKKGINTLINMSRLGQDDPTPSRINNHRELEFLGDVVEFLTSTV 982
DB RQPKYGRKVVHMRKKGINTLINMSRLGQDDPTPSRINNHRELEFLGDVVEFLTSTV 839

QY 983 HLYVLPSPLEGGATVTRTAIVQNOHLAMAKKLELDPMLYAHGPDLCRESDLRHMAN 1042
DB HLYVLPSPLEGGATVTRTAIVQNOHLAMAKKLELDRFMLYAHGPDLCRESDLRHMAN 899

QY 1043 CFEALIGAVYLEGSLEAKQLFGRLLFNDPDLREVWMLNYPHLPLQOEPTNDQLIETSP 1102

DB 900 CFEALIGAVYLEGSLEAKQLFGRLLFNDPDLREVWMLNYPHLPLQOEPTNDQLIETSP 959
QY 1103 VLQKLEFEFEAIGVIFTHVRELLARAFTRTVGNHNLTLGHNQRMFLGDSIMQLVATEYL 1162
DB VLQKLEFEFEAIGVIFTHVRELLARAFTRTVGNHNLTLGHNQRMFLGDSIMQLVATEYL 1019
QY 1163 FIHPDPHGHLLTLRSSLVNNRTQAKVABELGMOEYAITNDKTRPVGLRKTTLADLLE 1222
DB FIHPDPHGHLLTLRSSLVNNRTQAKVABELGMOEYAITNDKTRPVGLRKTTLADLLE 1079
QY 1223 SFTAALYTDKLEYVHTFMNVCFPRLKBPILNQDNDPKSQLOQCCLTLRTEGKEPDIP 1282
DB SFTAALYTDKLEYVHTFMNVCFPRLKBPILNQDNDPKSQLOQCCLTLRTEGKEPDIP 1139
QY 1283 LYKTLQTVGSHARTTVAVYFKGERIGCGKGPSIQOAEAGAAAMDALEKYNFPQMAHQKR 1342
DB LYKTLQTVGSHARTTVAVYFKGERIGCGKGPSIQOAEAGAAAMDALEKYNFPQMAHQKR 1199
QY 1343 FIOKRYOELKEMWREHREHOREPDETDIKK 1374
DB FIOKRYOELKEMWREHREHOREPDETDIKK 1231

RESULT 4

QSZIR3_CHICK
ID QSZIR3_CHICK PRELIMINARY; PRT; 1336 AA.
AC QSZIR3;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCJMB04_24a21;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatki A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis."
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ270721; CAG32380.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003725; F:double-stranded RNA binding; IEA.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004525; F:ribonuclease III activity; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR000999; RNase_III.
DR Pfam; PF00035; dsrm; 1.
DR Pfam; PF00636; Ribonuclease_3; 2.
DR SMART; SM00358; DSRM; 1.
DR SMART; SM00535; RIBOC; 2.
DR PROSITE; PS00137; DS_RBD; 1.
DR PROSITE; PS00517; RNASE_3_1; 2.
DR PROSITE; PS00142; RNASE_3_2; 2.
KW Hypothetical protein.
SQ SEQUENCE 1336 AA; 154836 MW; 50D9A9AC53DE0CF CRC64;

Query Match 84.6%; Score 6344.5; DB 2; Length 1336;
Best Local Similarity 85.3%; Pred. No. 1.7e-301;
Matches 1171; Conservative 76; Mismatches 81; Indels 45; Gaps 5;

QY 10 MSPHGRGPRGRGGHARGAPSPFRPNRLHLPQPPVQYQYPPSPSTFSPSPAP 69
DB 1 MSPHGRGPRGRGGHARGAPSPFRPNRLHLPQPPVQYQYPPSPSTFSPSPAP 60

Db 53 ----- 52
Qy 182 PNFQNPSSFLPSANNSSPHFLPLPYPLPKAPSERRSPERLKHYYDDHRHDHSHGRG 241
Db 53 ----- 52
Qy 242 ERHSLDRRGRSPDRRRQDSRYSDYDRGTPSRHRSYERSRERERHRHRDNRSP 301
Db 53 ----- 52
Qy 302 SLERSYKKEYKRSGRSYGLSVVPACGTPELPGEIIKNKTDSWAPPLEIVNHRSPSREKK 361
Db 53 ----- 52
Qy 362 RARWEEKDRWSDNQSGKDKNYTSIKEKEPEETMPDKNBEEBELLKPVWIRCTHSENY 421
Db 53 ----- 68
Qy 422 YSSDPMQVGDSTVVGTSRLRLDLYDFEELGSRQEKAKARPWPBPPTKLDLEDLESS 481
Db 69 YSSDPMQVGDSTVVGTSGLRLDLYDFEELGSRQEKAKARPWPBPPTKLDLEDLESS 128
Qy 482 ESECESEDESDSCSSSSDSEFVIAEIKRKAHPDRLHDELWYNDPGQMDGFLCKCSAK 541
Db 129 ESECEDESDSCSSSSDSEFVIAEIKRKAHPDRLHDELWYNDPGQMDGFLCKCSAK 188
Qy 542 ARRTGIRHSYPGEEAIKPCRPMTNAGRLPHYRITVSPPTNFLTDRPTVIEDDHIYIF 601
Db 189 ARRTGIRHSYPGEEAIKPCRPMTNAGRLPHYRITVSPPTNFLTDRPTVIEDDHIYIF 248
Qy 602 EGSFMAFAHPLTNPLCKVIRFNIDYTHFIEEMWPNFCVKGLESLFLFDDILELYD 661
Db 249 EGSFMAFAHPLTNPLCKVIRFNIDYTHFIEEMWPNFCVKGLESLFLFDDILELYD 308
Qy 662 WNLKGPLFEDSPCCPFHMPFRVFLPDGGEVLSMHQILLYLRCSKALYPBEEIAN 721
Db 309 WNLKGPLFEDSPCCPFHMPFRVFLPDGGEVLSMHQILLYLRCSKALYPBEEIAN 368
Qy 722 MLQWEELEWQYAECKGMIVTPGTPSSVRIDQDREQFNPDVITFPPIIVHFGIRPAQ 781
Db 369 MLQWEELEWQYAECKGMIVTPGTPSSVRIDQDREQFNPDVITFPPIIVHFGIRPAQ 428
Qy 782 LSVAGDPQYOKLWKSYYKLRLHLANSKVKQTDQKLAOREEALQKIQKNTWRREVTV 841
Db 429 LSVAGDPQYOKLWKSYYKLRLHLANSKVKQTDQKLAOREEALQKIQKNTWRREVTV 488
Qy 842 LSSQGFWKTIQIRSDVCOHAMMLPVLTHIRYHQCMLHLDKLGIVTFQDRCLLQAMTHPS 901
Db 489 LSSQGFWKTIQIRSDVCOHAMMLPVLTHIRYHQCMLHLDKLGIVTFQDRCLLQAMTHPS 548
Qy 902 HHLNFGMNPDPHARNSLSNCGIRQPKYGDGRKVHMHMRKKGINTLINIMSLRGQDDPTPSR 961
Db 549 HHLNFGMNPDPHARNSLSNCGIRQPKYGDGRKVHMHMRKKGINTLINIVSLRGQDDPTPSR 608
Qy 962 INHNERLEFLGDVAVFELTSVHLIYLPSPSEEGLATYRTAIVQNOHMLAKKGLDLPF 1021
Db 609 INHNERLEFLGDVAVFELTSVHLIYLPSPSEEGLATYRTAIVQNOHMLAKKGLDLPF 668
Qy 1022 MLYAHGPDLCRESDLRHAMANCEALIGAVYLGESLEAKQLFGRLLFNDPDLREVWLN 1081
Db 669 MLYAHGPDLCRESDLRHAMANCEALIGAVYLGESLEAKQLFGRLLFNDPDLREVWLN 728
Qy 1082 PLHPLQIQEPNTDQLIETSPVLQKTEFEPEAIGVIFTHVRLLARAFPTLRTVGFNHLTLG 1141
Db 729 PLHPLQIQEPNTDQLIETSPVLQKTEFEPEAIGVIFTHVRLLARAFPTLRTVGFNHLTLG 788
Qy 1142 HNORMEFLGDSINQLVATEVLFTHFPDHHGCHTLIRSSLVNRRTOAKVAEELGMQEYAI 1201
Db 789 HNORMEFLGDSINQLVATEVLFTHFPDHHGCHTLIRSSLVNRRTOAKVAEELGMQEYAI 848
Qy 1202 TNDTKTRPVGLRTKTLADLLESFIAALYTDKDLVYVHTFMNVCFPPRLKFIINQDNDP 1261
Db 849 TNDTKTRPVGLRTKTLADLLESFIAALYTDKDLVYVHTFMNVCFPPRLKFIINQDNDP 908

Qy 1262 KSOLQOCCLTLRTEGKEPDIPLYKTLQTVGSPHARTYTVAVYFKGIRGCKGPSIOQAE 1321
Db 909 KSOLQOCCLTLRTEGKEPDIPLYKTLQTVGSPHARTYTVAVYFKGIRGCKGPSIOQAE 968
Qy 1322 MGAAMDALEKYNFPQMAHQKRFICRYQBELKEMWEREHQEREPEDETDIKK 1374
Db 969 MGAAMDALEKYNFPQMAHQKRFICRYQBELKEMWEREHQEREPEDETDIKK 1021

RESULT 6

Q6PF88 MOUSE
ID Q6PF88 MOUSE PRELIMINARY; PRT; 942 AA.
AC Q6PF88
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Rnasen protein (Fragment).
GN Names=Etoh12; Synonyms=Rnasen;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Heih F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RG NIH MGC Project;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057687; AAH57687.1; -, mRNA.
DR Ensembl; ENSMUSG00000022191; Mus musculus.
DR MGI; MGI:1261425; Etoh12.
DR MGI; MGI:1261425; Rnasen.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003725; F:double-stranded RNA binding; IEA.
DR GO; GO:0004525; F:ribonuclease III activity; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR InterPro; IPR001159; Da RNA bd.
DR InterPro; IPR000999; Rnasen III.
DR Pfam; PF00035; dazm; 1.
DR Pfam; PF00636; Ribonuclease_3; 2.
DR SMART; SM00358; DSRM; 1.
DR SMART; SM00535; RIBOC; 2.
DR PROSITE; PS00137; DS RBD; 1.
DR PROSITE; PS00517; RNASE_3_1; 2.
DR PROSITE; PS0142; RNASE_3_2; 2.
FT NON_TER 1 1

SQ	SEQUENCE	942 AA; 109445 MW; C3629E4676F6C8B CRC64;	
	Query Match	56.4%; Score 4982; DB 2; Length 942;	
	Best Local Similarity	98.9%; Pred. No. 4.1e-235;	
	Matches 932; Conservative	5; Mismatches 5; Indels 0; Gaps 0;	
QY	433	STVVGTSRLRLDYKFEELGSRQEKAKARPPEPPKTKLDRDLSSSESECEDESDT	492
DB	1	STVVGTSRLRLDYKFEELGSRQEKAKARPPEPPKTKLDRDLSSSESECEDESDT	60
QY	493	CSSSSDSEVDVIAETIKRKAHPDRHLDELWYNDPQMDNGPLCKCSAKARTGIRHSIY	552
DB	61	CSSSSDSEVDVIAETIKRKAHPDRHLDELWYNDPQMDNGPLCKCSAKARTGIRHSIY	120
QY	553	PGEEAIKPCRPMTNNAAGRLPHYRIITVSPPTNFITDRPTVIEYDDHEVIEFEGSMFAHPL	612
DB	121	PGEEAIKPCRPMTNNAAGRLPHYRIITVSPPTNFITDRPTVIEYDDHEVIEFEGSMFAHPL	180
QY	613	TNIPLCVKVIRFNIDYTIHFIEEMMPENFCVKGLELSFLFRDILELYDWNKGPFLFDS	672
DB	181	TNIPLCVKVIRFNIDYTIHFIEEMMPENFCVKGLELSFLFRDILELYDWNKGPFLFDS	240
QY	673	PPCCPRFHMPPRVFLPDGKKEVLSMHQIILLYLLRCSKALVPEEBIANMLQWEELEWQK	732
DB	241	PPCCPRFHMPPRVFLPDGKKEVLSMHQIILLYLLRCSKALVPEEBIANMLQWEELEWQK	300
QY	733	YABECKGMIVNPGTSPSSVRIDQLDREQFNPEVITFPIIVHFGIRPAQLSVAGDPQYOK	792
DB	301	YABECKGMIVNPGTSPSSVRIDQLDREQFNPEVITFPIIVHFGIRPAQLSVAGDPQYOK	360
QY	793	LWKSYYKLRLHLANSPKVQTKDQKLAQREELQKLRQNTWRREVTVLSSQGFWKGTGI	852
DB	361	LWKSYYKLRLHLANSPKVQTKDQKLAQREELQKLRQNTWRREVTVLSSQGFWKGTGI	420
QY	853	RSVQCQHAMWLPVLTTHIRHYOCIMHLDKLIIGYTFQDRCLLQAMTHPSHLNFGMNPDH	912
DB	421	RSVQCQHAMWLPVLTTHIRHYOCIMHLDKLIIGYTFQDRCLLQAMTHPSHLNFGMNPDH	480
QY	913	ARNLSNCGIRQPKYGDVKVHHMKKGINTLINMSRLGDDPTPSRINNNERLEFLG	972
DB	481	ARNLSNCGIRQPKYGDVKVHHMKKGINTLINMSRLGDDPTPSRINNNERLEFLG	540
QY	973	DAVVEFLTSVHLVYLPSPLEEGGLATRTAIVONQHLAMAKKLEDPFMYAHGPDLCR	1032
DB	541	DAVVEFLTSVHLVYLPSPLEEGGLATRTAIVONQHLAMAKKLEDPFMYAHGPDLCR	600
QY	1033	ESDLRHAMANCFEALIGAVYLEGSLEAKQLFGRLLFNDPDLREVWLNYPHLPLQOEPN	1092
DB	601	ESDLRHAMANCFEALIGAVYLEGSLEAKQLFGRLLFNDPDLREVWLNYPHLPLQOEPN	660
QY	1093	TRQLIETSPVLQKLTFFESAIGVITFHVLLARAFITRTVGNHLLTLGHNQRMFLGDS	1152
DB	661	TRQLIETSPVLQKLTFFESAIGVITFHVLLARAFITRTVGNHLLTLGHNQRMFLGDS	720
QY	1153	IMOLVATEYLFIFPDHHEGHTLLRSSLVNNRTQAKVABELGQVYAINDTKTKPVGL	1212
DB	721	IMOLVATEYLFIFPDHHEGHTLLRSSLVNNRTQAKVABELGQVYAINDTKTKPVGL	780
QY	1213	RTKTLADLLESFIAALYTDKXLEYVHTFMNVCFPPRLKEFIFLNQDWNDDPKSQIQQCCLTL	1272
DB	781	RTKTLADLLESFIAALYTDKXLEYVHTFMNVCFPPRLKEFIFLNQDWNDDPKSQIQQCCLTL	840
QY	1273	RTSGKGPDIPLYKTQTVGSHARTYTVAVYFGERIGCGKGPSIOAENGAMDALEKY	1332
DB	841	RTSGKGPDIPLYKTQTVGSHARTYTVAVYFGERIGCGKGPSIOAENGAMDALEKY	900
QY	1333	NFPQAHQKRFYGRYQELKEMRWREHOREPDETEDEIKK	1374
DB	901	NFPQAHQKRFYGRYQELKEMRWREHOREPDETEDEIKK	942

RESULT 7
.Q7TWI8_MOUSE

ID	Q7TWI8_MOUSE PRELIMINARY;	PRT; 780 AA.
AC	Q7TWI8;	
DT	01-OCT-2003 (tREMBLrel. 25, Created)	
DT	01-OCT-2003 (tREMBLrel. 25, Last sequence update)	
DT	01-MAR-2004 (tREMBLrel. 26, Last annotation update)	
DE	Rnaen protein (Fragment).	
GN	Name=Etchi2; Synonyms=Rnaen;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	
OC	Muroidea; Muridae; Murinae; Mus.	
OX	NCBI_Taxid=10090;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6; TISSUE=Mouse;	
RX	MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,	
RA	Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6; TISSUE=Mouse;	
RG	NIH MGC Project;	
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC055696; AAH55696.1; -; mRNA.	
DR	HSSP; O67082; 1JFZ.	
DR	Ensembl; ENSMUSG0000022191; Mus musculus.	
DR	MGI; MGI:1361425; Etchi2.	
DR	MGI; MGI:1361425; Rnaen.	
DR	GO; GO:0003622; C:intracellular; IEA.	
DR	GO; GO:0003725; F:double-stranded RNA binding; IEA.	
DR	GO; GO:0004525; F:ribonuclease III activity; IEA.	
DR	GO; GO:0006396; P:RNA processing; IEA.	
DR	InterPro; IPR001159; ds_RNA_bd.	
DR	InterPro; IPR000999; RNase_III.	
DR	Pfam; PF00035; dsrm; 1.	
DR	SMART; SM00358; DSRM; 1.	
DR	SMART; SM00535; RIBOC; 2.	
DR	PROSITE; PS00137; DS_RBD; 1.	
DR	PROSITE; PS00517; RNASE_3_1; 2.	
DR	PROSITE; PS00142; RNASE_3_2; 2.	
FT	NON_TER	
SQ	SEQUENCE 780 AA; 91045 MW; 78D734332C75382E CRC64;	

Query Match	54.9%;	Score 4121; DB 2; Length 780;
Best Local Similarity	99.1%;	Pred. No. 3.8e-193;
Matches 773; Conservative	2; Mismatches 5; Indels 0; Gaps 0;	
QY	595	DDHEYIFEGFSFAHAPLTNIPLCVKVIRFNIDYTIHFIEEMMPENFCVKGLELSFLFR 654
DB	1	DDHEYIFEGFSFAHAPLTNIPLCVKVIRFNIDYTIHFIEEMMPENFCVKGLELSFLFR 60
QY	655	DILELYDWNKGPFLFDSPPCCPRFHMPPRVFLPDGKKEVLSMHQIILLYLLRCSKALV 714
DB	61	DILELYDWNKGPFLFDSPPCCPRFHMPPRVFLPDGKKEVLSMHQIILLYLLRCSKALV 120

QY 715 PEEIANNLOWERLEWQYAECKGMIIVTNGTKPSVRIDQLDRQPNPDVITPFIIVH 774
 DB 121 PEEIANNLOWERLEWQYAECKGMIIVTNGTKPSVRIDQLDRQPNPDVITPFIIVH 180
 QY 775 FGIRPAQLSVAGDPQYQKWLKSVVKKLHLLANSVKVKQTDKQKLAQREELAQIKRQNTM 834
 DB 181 FGIRPAQLSVAGDPQYQKWLKSVVKKLHLLANSVKVKQTDKQKLAQREELAQIKRQNTM 240
 QY 835 RREVTVELSSQGWKTKGIRSDVCOHAMMLPVLTHIRYHQLMHLDKLIGYTFQDRCLLQ 894
 DB 241 RREVTVELSSQGWKTKGIRSDVCOHAMMLPVLTHIRYHQLMHLDKLIGYTFQDRCLLQ 300
 QY 895 LAMTHSHLHPCWNPDPHARNLSNCGIRPKYGDRAKVVHMMKKGINTLINIMSRGQ 954
 DB 301 LAMTHSHLHPCWNPDPHARNLSNCGIRPKYGDRAKVVHMMKKGINTLINIMSRGQ 360
 QY 955 DDPTPSRINNEERLEFLGDAVVEFLTSVHLIYLPSPLEEGGLATYRTAIVQNOHLAMLA 1014
 DB 361 DDPTPSRINNEERLEFLGDAVVEFLTSVHLIYLPSPLEEGGLATYRTAIVQNOHLAMLA 420
 QY 1015 KLELDPFMYAHGPDLCRESDLRHAMANCEALIGAVYLEGSLEBAKQLFGRLLFNDPDL 1074
 DB 421 KLELDPFMYAHGPDLCRESDLRHAMANCEALIGAVYLEGSLEBAKQLFGRLLFNDPDL 480
 QY 1075 REVWLYPLHPLQLOPNTDRQLIETSPVLQKLTETFEBAIGVITFVRLARAFITLRTVG 1134
 DB 481 REVWLYPLHPLQLOPNTDRQLIETSPVLQKLTETFEBAIGVITFVRLARAFITLRTVG 540
 QY 1135 FNLHTLGHNMREFLGDSTMLQVATVFLTHPPDHHEGLHTLRSLSVNNRTQAKVABE 1194
 DB 541 FNLHTLGHNMREFLGDSTMLQVATVFLTHPPDHHEGLHTLRSLSVNNRTQAKVABE 600
 QY 1195 GMOEYAITNDKTRPVGLRTKTLADLLESFIAALYTDKOLEYVHTFMVVCFFPRLKEFIL 1254
 DB 601 GMOEYAITNDKTRPVGLRTKTLADLLESFIAALYTDKOLEYVHTFMVVCFFPRLKEFIL 660
 QY 1255 NQDNDPKSQLOCCLTLTREGKEPDIPLYKTLQTVGPHSHARTYTVAVTFKGRICGGKG 1314
 DB 661 NQDNDPKSQLOCCLTLTREGKEPDIPLYKTLQTVGPHSHARTYTVAVTFKGRICGGKG 720
 QY 1315 PSTQQAEMGAAMDALKYPPMAHOKRFRIGRYOELKEMWEREHOEPDETEDIK 1374
 DB 721 PSTQQAEMGAAMDALKYPPMAHOKRFRIGRYOELKEMWEREHOEPDEAEDIK 780
 RESULT 8
 Q4SKW1_TETNG PRELIMINARY; PRT; 1041 AA.
 AC Q4SKW1;
 DT 13-SEP-2005 (TEMBLrel. 31, Created)
 DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAFL4565, whole genome shotgun sequence.
 GN ORNames=GSTENG00016530001;
 OS Tetraodon nigroviridis (green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_Taxid=99883;
 RN NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli S., Bouneau L., Fischer C., Ozouf-Coataz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN NUCLEOTIDE SEQUENCE.
 RP Genoscope; Whitehead Institute Centre for Genome Research;
 RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 RL -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAE01014565; CAF98721.1; -: Genomic DNA.
 SQ SEQUENCE 1041 AA; 120534 MW; 2CA7AL65A7BB3CDB CRC64;
 Query Match 50.2%; Score 3767; DB 2; Length 1041;
 Best Local Similarity 67.5%; Pred. No. 1.1e-175;
 Matches 738; Conservative 80; Mismatches 135; Indels 140; Gaps 18;
 QY 10 MSFHPGCGPCRGCGHGAAPSAPSPQNLRLHLPQPPVQYQYEPSPASTTF-SNSPA 68
 DB 1 MSFHQDRAAHREPCMAFGPHMSPQNTYRPTNLRPQPQPPVPPHYDPQVPSSGYHSNS-- 58
 QY 69 PNFLLPRPDPVPPPP-----PMPESAQGP-LPPCPIRPPFPNHHMRHPPFPVPPC 116
 DB 59 -GTMHPHSTFMQVSPGAFADSRSEPVPAQBGPHLPCLPRTPTSLYMMHPVPPPLA 117
 QY 117 FPPMPPPMPCPN---NPPVPGAPPGQGTFFFMMPPPSMHPPPPPVMPQOVNYQYPPGS 173
 DB 118 RPPMPAPIHSPMSYHPPY-----PMNSPHPPHP----- 147
 QY 174 HNFPPPPSPNS-FQNNPSSFLPSANNSSPHFHLPPYLPKAPSRERRPERLKHVDDHR 232
 DB 148 ---FPPPTFNSGHVQSPGSAFDLG-----FHHGGFYKHKDPADKRRSPERGHRDDL 198
 QY 233 HRDHS-GRGERHSL---DRRERGRSPDR--RRDSTRVSDYDRGRTSRHRSYERSRE 286
 DB 199 QGYSHSGHSDKQMEFFGDRKDRGSPDRWRPEGGRHRSYDRGRTTPRH-----RSRE 254
 QY 287 RERERHRRHNRSSPSLERSYKKEYKRSRGSYGLSVVPEPAGCTPELPGELIKNTDSWAP 346
 DB 255 RSERYVHRDSSRSQSPDRHRKPRSRSG----- 283
 QY 347 PLIEVNHRSRREKRGARWEEKDRWSDNQSS-GDKNTSTIKKEPTEMTPK----- 399
 DB 284 -----SRERKSRWEEERRERSSSAPSRSRSYVSARNRDSSEAVPERERGFP 333
 QY 400 -----NEEEEEEELKPVWIRCTHSENYSSDPMDQVGDSTVVG 438
 DB 334 TRGREGEPPALPHDREKEKEEKEEELKPAWIKTHAESYSDNDMDQVGDSTVVG 393
 QY 439 SRLRLDYKFEBELAGSRQKAKAAPPPWPPPKTKLDEDL-ESSSESECESED-STCSS 496
 DB 394 SKLRDLYQRFEEELGRRQARAKAAPKWEPPKTKLDEDPDESSESECESEDADSTCSS 453
 QY 497 SDESEVDVTAIEIKRKAHPDRHLDELWYNDPGMNDGPKCKCSAKARRTGIHRSIYPGE 556
 DB 454 SDDSDVDVTAIEIKRKAHPDRHLDELWYNDPGMNDGPKCKCSAKARRTGIHRSIYPGE 513
 QY 557 AIKPCPMTNNAAGRLPHYRITVSPPTNFLTDRPTVLEYDDHEVIFEGFSWFAHPLTNIP 616
 DB 514 SVKQCRAMNNAGKLFHYRITVSPPTNFLTDRPTVLEYDDHEVIFEGFSWFAHPLTNIP 573
 QY 617 LCKVTRFNIDYTHIFTEEMMPENFCVKGLFSLFLFRDLILELYDNWLGKPLPEDSPCC 676
 DB 574 LCRVTRFNIDYTHIFTEEMTPENYCVRGLELFSYLFQDILELYDNWLGKPLPEDSPCC 633
 QY 677 PRFHMPFRVRLPGGKEVLSMHQILLYLLRCSSKALVPEEETIANMLQWEELEWQYAE 736
 DB 634 PQFHMPFRVRLPGGKEVLSMHQVLLYLLRSSKPLVPEEETIADMLQWEELEWQYAE 693
 QY 737 CKGMIVTNGTVPSSVRIDOLAREQNPVITPFIIVHFGIRPAQLSVAGDPQYQKWLK 796

694 CKGMIVTNGMKPSSVRIDQLDREQFNPVDVITPPIIVHFGIRPAQLSYAGDPQYQKLMKS 753

797 YVKLRHLLANSKPVKQTDQKLAQREALQKIQKNTMRREVTVLSSQGFWKGTGRSDY 856

754 YVKLRHLLANSKPVKQIDQKLMQREALQKIQKNTMRREVTVLSSQGFWKSGIRSDV 813

857 CQHAWMLPVLTHIRYHQCMLHLDKLGITTFODRCLLQALWTHPSHHLNFGWNPDHARNS 916

814 CQHAWMLPVLTHIRYHQCMLHLDLQIGVYFTRCCLLQALWTHPSHHLNFGWNPDHARNS 873

917 LSNCGIRQPKYGDRKVVHMHMRKKGINTLINIMSLRGQDDPTPSRINHNHRLFLGDAVY 976

874 LSNCGIRQPKYGDRKVVHMHMRKKGINTLINIMSLRGQDDPTPSRINHNHRLFLGDAVY 933

977 EFLTSVHLVYLPSPLEEGGLATYRTAIVONQHMLAKKLELDPFMYAHGDPDLCSDDL 1036

934 EFLTSVHLVYLPSPLEEGGLATYRTAIVONQHMLAKKLELDRFMLYAHGDPDLCSDDL 993

1037 RHAWANCFEALIG 1049

994 RHAWANCFEALIG 1006

RESULT 9

Q80UUS MOUSE

ID Q80UUS_MOUSE PRELIMINARY; PRT; 705 AA.

AC Q80UUS;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Rnaesin Protein (Fragment).

GN NamesEtoh12; SynonymsRnaesin;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=129/Sv x 129/Sv-CP; TISSUE=ES Cell;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S., Krzywinski M.I., Skaleka U., Smalilus D.E.,

RA "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=129/Sv x 129/Sv-CP; TISSUE=ES Cell;

RG NTH MGC Project;

RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

DR ENBL; BC050057; AAH50057.1; -; mRNA.

DR HSSP; O67082; IJFZ.

DR Ensembl; ENSMUSG00000022191; Mus musculus.

DR MGI; MGI:1261425; Etoh12.

DR MGI; MGI:1261425; Rnaesin.

DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:0003725; F:double-stranded RNA binding; IEA.

DR GO; GO:0004525; F:ribonuclease III activity; IEA.

DR GO; GO:0006396; P:RNA processing; IEA.

DR InterPro; IPR001159; Ds_RNA_bd.

DR InterPro; IPR000999; RNaase_III.

DR Pfam; PF00035; dsrm; 1.

DR Pfam; PF00636; Ribonuclease_3; 2.

DR SMART; SM00358; DSRM; 1.

DR SMART; SM00535; RIBOC; 2.

DR PROSITE; PS0137; DS_RBD; 1.

DR PROSITE; PS00517; RNASE_3_1; 2.

DR PROSITE; PS0142; RNASE_3_2; 2.

FT NON_TER 1

SQ SEQUENCE 705 AA; 82084 MW; 3332C69A5F1977D6 CRC64;

Query Match 49.3%; Score 3696; DB 2; Length 705;

Best Local Similarity 98.7%; Pred. No. 2e-172; Indels 0; Gaps 0;

Matches 696; Conservative 2; Mismatches 7;

QY 670 EDSPPCCPRFHPMPRFVRLPDGKKEVLSMHQILLYLLRCSKALVPEEIIANMLQWEELE 729

DB 1 EDSPPCCPRFHPMPRFVRLPDGKKEVLSMHQILLYLLRCSKALVPEEIIANMLQWEELE 60

QY 730 WQKYAECKGMIVTNPPTGTPSSVRIDQLDREQFNPVDVITPPIIVHFGIRPAQLSYAGDPQ 789

DB 61 WQKYAECKGMIVTNPPTGTPSSVRIDQLDREQFNPVDVITPPIIVHFGIRPAQLSYAGDPQ 120

QY 790 YOKLWKSYYKLRHLLANSKPVKQTDQKLAQREALQKIQKNTMRREVTVLSSQGFWK 849

DB 121 YOKLWKSYYKLRHLLANSKPVKQTDQKLAQREALQKIQKNTMRREVTVLSSQGFWK 180

QY 850 TGIKSDVDCQHAWMLPVLTHIRYHQCMLHLDKLGITTFODRCLLQALWTHPSHHLNFGMN 909

DB 181 TGIKSDVDCQHAWMLPVLTHIRYHQCMLHLDKLGITTFODRCLLQALWTHPSHHLNFGMN 240

QY 910 PHARNLSNCGIRQPKYGDRKVVHMHMRKKGINTLINIMSLRGQDDPTPSRINHNHRL 969

DB 241 PHARNLSNCGIRQPKYGDRKVVHMHMRKKGINTLINIMSLRGQDDPTPSRINHNHRL 300

QY 970 FLGDAVVEFLTSVHLVYLPSPLEEGGLATYRTAIVONQHMLAKKLELDPFMYAHGPD 1029

DB 301 FLGDAVVEFLTSVHLVYLPSPLEEGGLATYRTAIVONQHMLAKKLELDRFMLYAHGPD 360

QY 1030 LCRESDLRHAMANCFEALIGAVVLEGSLBEAKQLFGRLLFNDPDLREVWMLNYPFLHPLQLQ 1089

DB 361 LCRESDLRHAMANCFEALIGAVVLEGSLBEAKQLFGRLLFNDPDLREVWMLNYPFLHPLQLQ 420

QY 1090 EPNTRDQLIETSPVLOKLTPEPEAIGVITFHVRLARAFILRTVGFNHLTLGHNRMEFL 1149

DB 421 EPNTRDQLIETSPVLOKLTPEPEAIGVITFHVRLARAFILRTVGFNHLTLGHNRMEFL 480

QY 1150 GDSIMOLVATEYLFTHFPDHHGHLLTLRSSLVNNRTQAKVAEELGQEVATINDTKTKRP 1209

DB 481 GDSIMOLVATEYLFTHFPDHHGHLLTLRSSLVNNRTQAKVAEELGQEVATINDTKTKRP 540

QY 1210 VGLRTKTLADLLESFIAALYTDKLEVYHTFMNVCFPRPKKEFILNODMNDPKSQLOQCC 1269

DB 541 VALRTKTLADLLESFIAALYTDKLEVYHTFMNVCFPRPKKEFILNODMNDPKSQLOQCC 600

QY 1270 LTLRTGKGPDIPLYKTLQTVGSHARTYTVAVYFGERIGCGKGSIOQAENGAMDAL 1329

DB 601 LTLRTGKGPDIPLYKTLQTVGSHARTYTVAVYFGERIGCGKGSIOQAENGAMDAL 660

QY 1330 EKYNFPQMAHOKRFICGRYQRELKEMWREHOREPDETEDEIKK 1374

DB 661 EKYNFPQMAHOKRFICGRYQRELKEMWREHOREPDETEDEIKK 705

RESULT 10

Q9XYN5_DROME

ID Q9XYN5_DROME PRELIMINARY; PRT; 1327 AA.

AC Q9XYN5;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

QY	502	-FD---VIAIEIKKKAHPDLHDLWYNDPQGMNDGPKCKCSAKARRTGIRHSIYPGERA	557
Db	118	EFEDCSMBELTAKIKHPIRLHLDVNDPGENMDGPKCSARSRTGIRHGKYPGEG	177
QY	558	IKPCREMTNAGRLFYHRTVSPPTNFLTDRPTVIEYDDHEVIFEGFSMAFAPLTNIP	617
Db	178	FPKCPISNNAADKLHYRITISPTNFLTPTIIRKHDQHEFLFEGFSLLAHEPIGELPT	237
QY	618	CKVIRNIIDYTHIFEMBPENFCVGLBLFSLFLPDRIDLELYDMNLKPLPDSPPCCP	677
Db	238	CKVIRENIYITLYIEQMPENFTIRELNLFORYLELLELWDFTVQ-PSGSGEDSSCP	296
QY	678	RHEMRFRVFLPDGCKEVLSHQIILLYLLRCSKALVPREEIANMLQWELEWQKYAEC	737
Db	297	CYHFLFRFRDLPDNGKEVLAMSEVLRYLLDNGSLVPDPMLKEMMDMSQNEWDYDV	356
QY	738	KGMIVTNPQTKSSVRIDQLDR-----EQNPDPVITFPIITHFGIRPAQLSVAGDPQ	789
Db	357	KGNVSNPGMKCSVRVDQLDRNVGDVPEANAIDENGLVHPVIVHGIKPPQLSVAGNPE	416
QY	790	YQKLMKSYKLRHLANSFKVQTDKQKLAQREALOKIRQKNTMREVTVELSSQGFWK	849
Db	417	YQKAMREYIKFRLHJANMSPKPEDKRLKLEAKENRLEEMQMGRMKNITIAVSAKAFH	476
QY	850	TGIRSDVCQHMMPLVLTTHIRYHQCIMHLDKLIYTFQDRCLLOLANTHPSHLLNFGN	909
Db	477	TGIMCDMVQHMLIPVLTGHLFRHSANLVIRYIGYFTNRYTLQALTHPSYKFNFGN	536
QY	910	PHARNSLNCGRQPKYQDKRVHMHMKKGINTLINIMSLRGQDDPTPSRINHNRL	969
Db	537	PHARNSLNCGRQPKYQDKRVHMHMKKGINTLINIMSLRGQDDPTPSRINHNRL	969
QY	970	FLGDVAVEFLTSVHLYLPPSLEEGGLATYRTAIVQNHMLAKKLELDPFMYLAHGP	1029
Db	597	FLGDVAVEFLTSVHLYLPPSLEEGGLATYRTAIVQNHMLAKKLELDPFMYLAHGP	1029
QY	1030	LCRESDLHAMANCFALIGAVYLEGSLAEAKQLFGRLLFNDPD-LREVLNYPHPLQ	1088
Db	657	LCHELELHALANCFALIGAVYLEGSLAEAKQLFGRLLFNDPD-LREVLNYPHPLQ	1088
QY	1089	QEPNTDRLQIETSPVLOKITEPEAIGVIFTHVLLARAFRTLVGFNHLTLGHNMREF	1148
Db	717	QEPNTDRLQIETSPVLOKITEPEAIGVIFTHVLLARAFRTLVGFNHLTLGHNMREF	1148
QY	1149	LGDSIMQVATEYLFTHFPDHEHGLTLRSLSSVNNRTQAKVAEELGMOEYAI-TNDTK	1207
Db	777	LGDTVLQCLSEVLYRHFPEHHEGLTLRSLSSVNNRTQAKVAEELGMOEYAI-TNDTK	1207
QY	1208	RPVGLRTKTLADLLESFIAALYTDKOLEYVHTPMNVCFPPRLKEPILNQDNDPKSQLO	1267
Db	835	--ADLTKDORADLEAFALYVDKLEYCEMFCHVCLFPRLQDFIMNQDNDPKSKLOQ	892
QY	1268	CCLTLRT-EGKEPDIPLYKTQTVGSHARTYVAVYFKGERIGCGKPSIOAEMGAAM	1326
Db	893	CCLTLRTMGGEPIIPVYKVIETGPTNTRVSVAVYFKGRKLCACADGHSIOAEMNAK	952
QY	1327	DALE--KYNFPQMAHOKRFTGRYQRE 1351	
Db	953	QALENSKLFQPLDQRRVIAQSLKQ 979	
RESULT 12			
Q8CJ74	MOUSE		
ID	Q8CJ74_MOUSE PRELIMINARY;	PRT;	541 AA.
AC	Q8CJ74;		
DT	01-MAR-2003 (T-EMBLrel. 23, Created)		
DT	01-MAR-2003 (T-EMBLrel. 23, Last sequence update)		
DT	01-OCT-2003 (T-EMBLrel. 23, Last annotation update)		
DE	Ribonuclease III.		
GN	Name-Etchi2; Synonyms-Rn3, Nnaasen;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		

RESULT 13

OC	Muroidea; Muridae; Murinae; Mus.		
OX	NCBI_TaxID-10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN-BALB/c; TISSUE=Brain;		
RA	Min K.-L., Galarneau A., Parniak M.A.;		
RL	Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF440766; RAN63637.1; -, mRNA.		
DR	HSSP; O67082; IJFZ.		
DR	Ensembl; ENSMUSG00000022191; Mus musculus.		
DR	MGI; MGI:1261425; Etchi2.		
DR	MGI; MGI:1261425; Nnaasen.		
DR	GO; GO:0005622; C:intracellular; IEA.		
DR	GO; GO:0003725; C:double-stranded RNA binding; IEA.		
DR	GO; GO:0004525; P:ribonuclease III activity; IEA.		
DR	GO; GO:0006396; P:RNA processing; IEA.		
DR	InterPro; IPR001159; Ds RNA bd.		
DR	InterPro; IPR000999; Rnaase_III.		
DR	Pfam; PF00035; dsm; 1.		
DR	Pfam; PF00636; Ribonuclease_3; 2.		
DR	SMART; SM00358; DSRM; 1.		
DR	SMART; SM00535; RIBOG; 2.		
DR	PROSITE; PS00137; DS_RBD; 1.		
DR	PROSITE; PS00517; RNASE_3_1; 2.		
DR	PROSITE; PS0142; RNASE_3_2; 2.		
SQ	SEQUENCE 541 AA; 63007 MW; DOAC652A0CE044F1 CRC64;		
Query Match 37.7%; Score 2825; DB 2; Length 541;			
Best Local Similarity 98.3%; Pred. No. 5e-130;			
Matches 532; Conservative 3; Mismatches 6; Indels 0; Gaps 0;			
QY	834	MRREVTVELSSQGFNKTGIRSDVCQHMMPLVLTTHIRYHQCIMHLDKLIYGFQDRCLL	893
Db	1	MRREVTVELSSQGFNKTGIRSDVCQHMMPLVLTTHIRYHQCIMHLDKLIYGFQDRCLL	60
QY	894	QLAMTHPSHLNFGMNPDHARNSLNCGRQPKYQDKRVHMHMKKGINTLINIMSLRG	953
Db	61	QLAMTHPSHLNFGMNPDHARNSLNCGRQPKYQDKRVHMHMKKGINTLINIMSLRG	120
QY	954	QDDPTPSRINHNRLERLEFLGDVAVEFLTSVHLYLPPSLEEGGLATYRTAIVQNHMLA	1013
Db	121	QDDPTPSRINHNRLERLEFLGDVAVEFLTSVHLYLPPSLEEGGLATYRTAIVQNHMLA	180
QY	1014	KKLELDPFMYLAHGPDLCHRESDLHAMANCFALIGAVYLEGSLAEAKQLFGRLLFNDPD	1073
Db	181	KKLELDPFMYLAHGPDLCHRESDLHAMANCFALIGAVYLEGSLAEAKQLFGRLLFNDPD	240
QY	1074	LREVLNYPHPLQLOEPNTDRLQIETSPVLOKITEPEAIGVIFTHVLLARAFRTLV	1133
Db	241	LREVLNYPHPLQLOEPNTDRLQIETSPVLOKITEPEAIGVIFTHVLLARAFRTLV	300
QY	1134	GFNHLTLGHNMREFLGDSIMQVATEYLFTHFPDHEHGLTLRSLSSVNNRTQAKVAE	1193
Db	301	GFNHLTLGHNMREFLGDSIMQVATEYLFTHFPDHEHGLTLRSLSSVNNRTQAKVAE	360
QY	1194	LGQSYAIVTNDKTPRGVLRKTTLADLLESFIAALYTDKOLEYVHTPMNVCFPPRLKEFI	1253
Db	361	LGQSYAIVTNDKTPRGVLRKTTLADLLESFIAALYTDKOLEYVHTPMNVCFPPRLKEFI	420
QY	1254	LNQDNDPKSQLOQCCLTLRTGKBPDIPLYKTQTVGSHARTYVAVYFKGERIGCGK	1313
Db	421	LNQDNDPKSQLOQCCLTLRTGKBPDIPLYKTQTVGSHARTYVAVYFKGERIGCGK	480
QY	1314	GPSIOAEMGAAMDALEKYNFPQMAHOKRFTGRYQRELEKEMWEREHOREPEDETDIK	1373
Db	481	GPSIOAEMGAAMDALEKYNFPQMAHOKRFTGRYQRELEKEMWEREHOREPEDETDIK	540
QY	1374	K 1374	
Db	541	K 541	

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Q960Y4_DROME
ID Q960Y4_DROME PRELIMINARY; PRT; 1071 AA.
AC
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LD2995P.
GN Name-droscha; ORFNames=CG8730;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Nephrolepidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY051775; AAK93199.1; -; mRNA.
DR HSSP; O67082; 1JFZ.
DR Ensembl; CG8730; Drosophila melanogaster.
DR FlyBase; FBgn0026722; CG8730.
DR FlyBase; FBgn0026722; droscha.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003725; F:double-stranded RNA binding; IEA.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004525; F:ribonuclease III activity; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR InterPro; IPR001159; DS_RBD.
DR InterPro; IPR000999; RNase_III.
DR Pfam; PF00035; dsxm; 1.
DR Pfam; PF00636; Ribonuclease_3; 2.
DR SMART; SM00358; DSRM; 1.
DR SMART; SM00535; RIBOC; 2.
DR PROSITE; PS50137; DS_RBD; 1.
DR PROSITE; PS00517; RNASE_3_1; 1.
DR PROSITE; PS50142; RNASE_3_2; 2.
SQ SEQUENCE 1071 AA; 123158 MW; 25B6C2AAADA5078B CRC64;

Query Match 37.5%; Score 2811.5; DB 2; Length 1071;
Best Local Similarity 54.6%; Pred. No. 5.3e-129;
Matches 545; Conservative 169; Mismatches 220; Indels 65; Gaps 15;

QY 412 WIRCTHSENYSDPMDQVGDSTVVGTSRLRDLYDKFEEELGSRQEKAKAARPPWPPKT 471
Db 14 WVRSSPAELYERTK-----SENEVRGARLQKLTFLDELLQRAKRVREKLPVYVPPR 69

QY 472 KL-----DEDLSESECEDESDSTCSSSDSEVFDV-----TAEIKRKKAHPD 516
Db 70 KARRRVCKHKHKEACSSSSSSDDSDSDA-----FKIEQCCMBELSKVKYQHPQ 119

QY 517 RLHDEIWNYPGOWNDGPKCKSAKARTGIRHSIYPGEBAIKPCPTMTNAGRLFYRI 576
Db 120 RVHADLWHNDAGEMNDGPKCRSAKRRIGIRGIYPGETGYKLCDFPNSSNAGKLFYRI 179

QY 577 TVSPPTNFLTDRPTVLEYDDHEVYFFGFSMAFAPLTNIPLCVKIRFNIDYTHFTBEMM 636
Db 180 STSPPTNFLTPTTIKHDHFEFFGFSLSHVRLSDLPVCKVIRFNIEYTYEIEEKM 239

QY 637 PENFCVKGLFLSFLFRDILEYLDWNLKGPL----FEDSPCCPRFPMFRFVRLPDG 692
Db 240 PENFTIHELDIFPKYLFHEHLELVDFNLMPNLPSGNVEES---CPAFHPPFRFVRLPDN 296

QY 693 GKEVLMSHQILLYLLRCSKALVPEEIEANMLQWBELEFWQYAECKGMIVTNFGTKPSV 752
Db 297 GKEVLAMVEVRLYLLDONSQALVERQQLHLNQISQSEWQNYVDFIKGLMVKFGYKPCSL 356

QY 753 RIQDLREQNPDV-----ITPTLIIVHFGIRPAQLSYAGDPQYQKWLKSYVKRLHL 803
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357 RVDQLDRN--NSDLPECVDRETGISHPAIVHFGICHQPLSYAGNPEYQKAWREYVYKRL 414
804 LANSKPKVQTDKQKLAQREALQKIQKNTMREVTVELSSQGFWKTRSDVCQHAML 863
415 MANMSPKSPFKDKLEKEQRLQEMRTQGRMKRNTVAISSEGFYRTGMCDVVQHAMI 474
864 PVLTHIRYHQCIMHLDKLGITTFODRCLLQALMTHPSHLNFGMPPDHARNSLNCGR 923
475 PVLTHIRYHQCIMHLDKLGITTFODRCLLQALMTHPSHLNFGMPPDHARNSLNCGR 934
924 QPKYGDGRKVVHMRKKGINTLINMSRLGQDDPTPSRINHNERLEFLGDVAVFEFTSVH 983
535 QPEYGDGRKIVHNTKRGINTLVSMRFGKEHETVSNITNERLEFLGDVAVFEFTSVH 994
984 LYLFPSPLEGGIATYRTAIVQNHMLAKLELDFPMLYAHGPDLCRESDLRHAWANC 1043
595 LFFMPPELEGGIATYRAAIVQNHMLAKLELDFPMLYAHGPDLCRESDLRHAWANC 654
1044 FEALIGAVLEGSLBEAKOLFGRLLF--NDPDLREVWLNYPHLPLQLOQBNTDRLIETSP 1102
655 FEALMGALLDGGIKVADVFTDALFRQDEKLLSIWKNLPEHPLQOEPLGDRSCIDSYR 714
715 VLKELTKFEDSIGIKFKIRLLARAFTRDSIGFTHLTLGNSQRLFLGDTVLQLICSEYL 774
1163 FIHPDHHGHULTLRSSLVNNTQAKVAEELGMQEYAI--TNDKTKRPGVLRKTLDL 1221
775 YRHFPEHGHLSLLRSSLVNNTQAKVAEELGMQEYAI--TNDKTKRPGVLRKTLDL 830
1222 ESFIAALYTDKLEYVHTFMVCFPRLEKEFLINQDNDPKSQLOQCCLTLRT--EGKEPD 1280
831 EAFGLGALYVDKGLLYCEQCHVCLFRLQLFIMNQDNDPKSKLOQCCLTLRTMDGEPD 890
1281 IPLYKTLQTVGFSHARTYTVAVYFKGICGCKGPSIQQAEMGAAMDALAEKYN--PPQMA 1338
891 IPYKVVVEASGPTNTRVYKVVAVFRSKRLATSSGSSIQQAEMGAAMDALAEKYN--PPQMA 950
1339 HOKRFGIRKYRQEL---KEMRWEREHOREPDETEDIKK 1374
951 HOKRVIKSIKQTGNELDNDSRQOE-----EKIKR 983

RESULT 14
Q7FNE9 ANOGA
ID Q7FNE9 ANOGA PRELIMINARY; PRT; 836 AA.
AC Q7FNE9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000011622 (Fragment).
GN ORFNames=ENSANG00000009133;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: the sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008964; EAA12298.3; -; Genomic_DNA.
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DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003725; F:double-stranded RNA binding; IEA.
DR GO: GO:0004519; F:endonuclease activity; IEA.
DR GO: GO:0004525; F:ribonuclease III activity; IEA.
DR GO: GO:0006396; P:RNA processing; IEA.
DR InterPro: IPR001159; DS RBD.
DR InterPro: IPR000999; RNase_III.
DR Pfam: PF00035; dsm; 1.
DR Pfam: PF00636; Ribonuclease_3; 2.
DR SMART: SM00358; DSRM; 1.
DR SMART: SM00535; RIBOC; 2.
DR PROSITE: PS00137; DS RBD; 1.
DR PROSITE: PS00517; RNase_3_1; 1.
DR PROSITE: PS00142; RNase_3_2; 2.
FT NON_TER 836 836
SQ SEQUENCE 836 AA; 96229 MW; 8D3E0BD04953877D CRC64;

Query Match 35.8%; Score 2683.5; DB 2; Length 836;
Best Local Similarity 59.28; Pred. No. 7e-123;
Matches 499; Conservative 143; Mismatches 182; Indels 19; Gaps 8;

QY 514 HPDLHDELWYNDGQNDGPKCKSAKARTGIRHSIYPGEBAIKPCRPMTNNAKRLPH 573
DB 1 HPLRLHVLWYNDGEMNDGPKCRSARSRTGIRHGKYPGESEFKCIPSNNAKLYH 60

QY 574 YRITVSPNTNLTDRPTVIBYDHEIYIFEGFSMPAHAPLTNIPCKVIRFNIDYTHFIE 633
DB 61 YRITISPTNLTKTPTIHKDQHEFLFEFGLSLAHEPIGELPTCKVIRENIEVITYIE 120

QY 634 EMMPENFCVKGLFSLFLFRDILEYDNLKGLPDSPPCPRFHFMPFRVFLPDGG 693
DB 121 EQPENFTIRELNFORYLRELELVDFTVQ-PSGSGEDSSCPCHFLFRFRDLPDNG 179

QY 694 KEVLSHQIILYLLRCSKALVPEEIANMLQWELEWQKVAECKGMIVTNGTKPSSVR 753
DB 180 KEVLAMSEVLYLLDNSGLVPDMLKEMDMQSNQWQDVYDKGVNSNPGMKCSVR 239

QY 754 IDQLDREQFNPVITPPIIVHFGIRPAQLSAGDPQYQKLWKSIVKLRHLANSKPKQT 813
DB 240 VQLDRNV--GDVPEANADENG-----YAGNPEYQKAWREYIKFRHLIANMSKPSFE 290

QY 814 DKQLAQREBAQKIRQKNTMRREVTVELSSQGFWKGTGIRSDVCOHAMMLPVLTHIRYH 873
DB 291 DRKLEAKENLREMRQGRKGNITAVSAKAFHRTGIMCDVMQVAMLPVLTGHLRFH 350

QY 874 QCLMHLDKLIGYFQDRCLLQALMTHPSHHLNFGMPPDHARNSLSCNGIRQPKYGRKVH 933
DB 351 RSLNVLERYIGYFTYRYTLQALMTHPSYKENFGTHPDHARNSLTNCGIRQPEYGRKH 410

QY 934 HMMRKKGINTLINIMSLRGQDDPTPSRINHNERLEFLGDVAVEPLTSHLYLPPSLBE 993
DB 411 YMNTRKGINTLISIMSRFKEHETDSNITHNERLSFLGDVAVEFTISHLFHMFPDLSE 470

QY 994 GGLATYRTALVQNHMLAKKLELDPFMYLHAGPDLCHESDLRHAMANCPEALIGAVYL 1053
DB 471 GGLATYRAALVQNHMLAVLAKKLELDFEFLYHAGSDLCHELELRHALANCPEALMGALL 530

QY 1054 EGSLEBAKOLFGRLLENDPD-LREVLNVLPLHLQEQNPDRQLTETSPLVQLTEREE 1112
DB 531 DGGIEVADRVAYALFOEDTLTGIVWNTFSPHPLQEQPLGDRKHHIDSEMUKTLTRFED 590

QY 1113 AIGVIFTHVRLARAFLTRVGFNHLTLGHNQMBFLGDSIMQLVATEYLFIFHPDHEG 1172
DB 591 SIGVQNHIRLLARAFTRDSIGFTNLTLGNSQRLFLGTVLQLICSEVLYRHFPEHGG 650

QY 1173 HLTLLRSSLVNNTQAKVAELGMQYAI-TNDKTRPVGLTRTKTLADLLESFIALYTD 1231
DB 651 HLSLLRSSLVNNTQAVVCDLGMTOYAVSNPK----ADLTKORADLLEAFGLALYVD 706

QY 1232 KDLVYHTFMVCFPRLEKEFTLNQNDPKSQLOQCCLTLRT-EGKEPDIPLYKTLQTV 1290
DB 707 KGLEICYEMCFVCLFRLQFIMNQDNDPKSKLQCCCLTLRTMDGGSPDIPVYKVIECT 766

Search completed: December 24, 2005, 00:58:47
Job time : 277 secs
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QY 1291 GPHARTYTVAVYFKGERICGKGPSIQQAEMGAAMDALE--KYNFPQMAHQRFGRKY 1348
DB 767 GPTNTVYVAVYFRGKRKLACADGHSIQQAEMNAKQALNSKDLFPQLDQRRVIAQSL 826

QY 1349 ROE 1351
DB 827 KRQ 829

RESULT 15
Q59FF9 HUMAN
ID Q59FF9_HUMAN PRELIMINARY; PRT; 432 AA.
AC Q59FF9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Nuclear RNase III Drosha variant (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209501; BAD92738.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 432 AA; 50659 MW; E5D811B6DD61251A CRC64;
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Query Match 30.6%; Score 2298; DB 2; Length 432;
Best Local Similarity 99.8%; Pred. No. 2.1e-104;
Matches 424; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 556 EAIKPCRPMTNNAKRLFHYRITVSPPTNLTDRPTVIEYDDHEIYIFEGFSMPAHAPLTNI 615
DB 7 QAIKPCRPMTNNAKRLFHYRITVSPPTNLTDRPTVIEYDDHEIYIFEGFSMPAHAPLTNI 66

QY 616 PLCKVIRFNIDYTHFIEEMMPENFCVKGLELFLSLFLFRDILEYDNLKGLPFDSPPC 675
DB 67 PLCKVIRFNIDYTHFIEEMMPENFCVKGLELFLSLFLFRDILEYDNLKGLPFDSPPC 126

QY 676 CRRFHFMPFRVFLPDGGKEVLSMHQIILYLLRCSKALVPEEIANMLQWELEWQKVAE 735
DB 127 CRRFHFMPFRVFLPDGGKEVLSMHQIILYLLRCSKALVPEEIANMLQWELEWQKVAE 186

QY 736 ECKGMIVTNPCTKPSVRIQDLDRSQFNPDVITFPIIVHFGIRPAQLSYAGDPQYQKLWK 795
DB 187 ECKGMIVTNPCTKPSVRIQDLDRSQFNPDVITFPIIVHFGIRPAQLSYAGDPQYQKLWK 246

QY 796 SYVKLRHLANSKPKVQTDQKLAQREBAQKIRQKNTMRREVTVELSSQGFWKGTGIRSD 855
DB 247 SYVKLRHLANSKPKVQTDQKLAQREBAQKIRQKNTMRREVTVELSSQGFWKGTGIRSD 306

QY 856 VCOHAMMLPVLTHIRYHOCLEMLDKLIGYTFQDRCLLQALMTHPSHHLNFGMNPDAH 915
DB 307 VCOHAMMLPVLTHIRYHOCLEMLDKLIGYTFQDRCLLQALMTHPSHHLNFGMNPDAH 366

QY 916 SILSNCGIRQPKYGRKRVHMMRKKGINTLINIMSLRGQDDPTPSRINHNERLEFLGDV 975
DB 367 SILSNCGIRQPKYGRKRVHMMRKKGINTLINIMSLRGQDDPTPSRINHNERLEFLGDV 426

QY 976 VEFLT 980
DB 427 VEFLT 431
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